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                                                                              AAQ65520 encodes a prostrate specific membrane antigen (PSM, AAR55097). The PSM coding sequence is useful for suppressing or modulating the metastatic ability of prostate tumour cells to grow, or for eliminating them. The protein is useful to identify or purify ligands of the Ag. It is also an attractive target for Ab-directed imaging and targeting of prostatic tumour deposits.

(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                    Prostate-specific membrane antigen and DNA encoding useful for detecting haematogenous micro-metastatic and for identifying ligands which bind to PSM Ag
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comprising implanting vascular cells into an immundeficient manual, establishing an immune response in the mammal, and assaying a characteristic to determine cell-mediated immunity in the mammal. The methods and compositions of the present invention are useful for the generation of a cellular immune response, in particular a CTL response, for treatment directly against a tumour neovasculature. They can also be used for making research models targeting tumour neovasculature. The present invention using the anti-angiogenesis approach takes advantage of the need of tumours to recruit a blood supply to support their continued growth. This approach aims to disrupt a tumour's supply of nutrients to cause it to die or at least limit its growth. This sequence represents a DNA associated with the neo-vascularure preparation for treatment of cancer described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evaluating cell-mediated immunity, in particular cytotoxic {\tt T} lymphocyte responses, by implanting vascular cells, useful for treatment and research models for directly targeting tumor neovasculature -
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immunity

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TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG CAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA CTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAAGTGCCCTACAATGTTGGACCTGGCT ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGATGGTTGGAATCTTCCTGGAGGTGGTG ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTG 839 1378 1318 659 1138 1498 1438 1258 1198 1078 419 1018 599 539 479 359 958 299

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CC response against a cell comprising a target antigen (I) in a subject, CC treating a subject having undesired cells, for example tumour cells CC or virally infected cells (C), reducing the number of (C) in a subject, CC and stimulating presentation of (I) by a cell. This is done by CC administering a polynucleotide (II) exocding a variant of (I), so that CC (II) expressed in a cell and cell-mediated immune response is induced. The method can be used to treat prostate cancer, breast cancer, Colorectal cancer and pancreatic cancer, as well as lymphomas and CC leukaemias. The method is also useful in treating chronic viral CC infections such as those caused by hepadnaviruses, lentiviruses and the CC including human immunodeficiency virus (HIV), herpesviruses and the Sequence of human prostate specific membrane antigen (PSMA) variant which has the signal sequence deleted, used as a target antigen in the

coding

Example 1;

Page 114-118;

146pp; English.

invention relates to a method of inducing a cell-mediated immune

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(first entry)

prostatic prostatic hyperplasia hyperplasia; gene BPH; #451 prostate cancer;

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                                                                                                                                                                                                                                                                                                                                                                                            cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
h; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
atic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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 2000US-233133P
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03-OCT-2000;
03-OCT-2000;
03-OCT-2000;
01-NOV-2000;
01-NOV-2000;
                                                                                                                                                                                anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, peschhangal cyarian vidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for anti-neoplastic agent involves exposing cells to chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature generation.
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Sequence 2653 BP; 782 A; 524 C; 640 G; 707 T; 0 other;

papillary carcinoma

and Wilm's tumour.

oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine

Query Match Best Local

Similarity

98.5%;

Score 1702.6;

DΒ

24;

Length

2653;

δõ Š Вb Q B Qγ В Matches 1729; 1079 1019 480 959 899 420 300 240 ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTG AGGTTAAAAATGCCCAGCTGGCAGGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTACC AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCCGACCCTGCTG CAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC Conservative 0; Pred. No. 0;
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          TTTCTGCAGTAAAAATTTTACAGAAATTGCTTCCAAGTTCAGCGAGAGACTCCAGGACT
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B 64 B 64

45 A

The present invention describes an isolated epitope (I) and an epitocluster. Also described is a vaccine or immunotherapeutic composit: (VC) comprising (I). (I) has cytostatic activity. VC is useful for treating an animal, by administering to an animal the vaccine or immunotherapeutic composition. VC is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic composition, by

composition

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07-NOV-2001;
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                            TGGTATACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC
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prostate

expression

marker

CDNA

(first

entry)

standard;

cDNA;

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                       CTCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCCCAGGAATTTATGATGCTCTGT
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a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

CC (e) assessing the efficacy of a therapy for inhibiting prostate cancer

CC (f) assessing the prostate cell carcino-

CC (g) determining whether normal carcino-

CC (h) assessing the prostate cell carcino-
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16-MAR-2000;
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09-JUN-2000;
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13-DEC-2000;
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; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
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tate cancer, stage
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
The invention relates to an isolated nucleic acid molecule (I) a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) c specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancel (b) monitoring the progression of prostate cancer in a patient.
                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate pharmacogenomic
                                                                                                   Claim
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Novel isolated prostate cells a for detecting p presence nucleic acid molecule associated with cancerous state of and correlating with presence of prostate cancer, useful presence of prostate cancer -

a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer, (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for a patient; (d) assessing the efficacy of a therapy for a patient; (d) assessing the efficacy of a therapy for a patient;

(g) dete
(h) asse
patient;
(I) is a selecting a composition for inhibiting prostate cancer i assessing the prostate cell carcinogenic potential of a determining whether prostate cancer has metastasized in assessing the aggressiveness or indolence of prostate can er in a patient;
f a compound;
in a patient;
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Length

Sequence 2884 BP; 851 Α; 551 Ç 684 <u>ი</u> 784 T; 14 other;

also

useful

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a pharmacodyanamic or

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Best Local Similarity
Matches 1729; Conserv
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The invention relates to an isolated nucleic acid molecule (I) a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) c specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cand

prostate cancer;

) comprising of the

Claim

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Page

6076-6077;

11750pp;

English

Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer

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                                                    AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTG
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ng the efficacy of a test compound to inhibit prostate
patient;
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Matches 1728
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24-FEB-1995;
02-JUN-1995;
                                                                                                                                                 A cDNA clone (AAT36785) codes for human 100 kDa prostate-specific membrane (PSM) antigen (AAW02234), an integral membrane glycoprotein that is very highly expressed in prostatic tumours and metastases. It was obtd. from lymph node carcinoma of prostate (LNCaP) cell mRNA by PCR amplification (see also AAT36795-808) and screening of an LNCaP cDNA library using an amplified cDNA partial clone as probe. The cDNA can be used to provide <u>Drobes</u> and primers useful e.g. in detecting hematogenous micrometastatic tumour cells and determining prostate cancer progression (see also AAT36827-30 and AAT36813-18), and in gene therapy. An alternatively spliced PSM, PSM', has a shorter cDNA sequence. PSM genomic DNA is given in AAT36786.
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                                                                                                                     Homo sapiens
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99US-0162506
99WO-US28313
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Best Local Similarity
Matches 1713; Conserv
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05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
                                                                                                                                     AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
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Ferrara N,
Goddard A,
Kljavin IJ
Shelton DI
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to target bioactive mol
cellular activities -
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                                                                                             2558 BP; 745 A; 509 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000WO-US00219.
; 2000WO-US00277.
; 2000WO-US00376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   des and polynucleotides used molecules to specific cells,
                        84.7%;
98.6%;
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Score 1687.2;
Pred. No. 0;
0; Mismatches
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Desnoyers L, Eaton I

Desnoyers L, Eaton I

Gurney AL, Hillan I

J, Paoni NF, Roy MA,

Illiams PM, Wood WI;
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1061 480 1120

1181 600 TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA 1240

1241 720 TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG

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GAGCATTTATTGATCCATTAGGGTTACCAGACAGACCTTTTTATAGGCATGTCATCTATG
                                                                                     GCAGAGGCACGGTATACTAAAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
                                                                                                                Human DNA encoding
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sapiens
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XX
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PD 20-SEP-2001.

28 - FEB-2001; 2001WO-US06520.

01 - MAR - 2000; 2000WO-US05601.
02 - MAR - 2000; 2000WS-1859541.
03 - MAR - 2000; 2000US-186958P.
14 - MAR - 2000; 2000US-189320P.
14 - MAR - 2000; 2000US-199328P.
15 - MAR - 2000; 2000US-199328P.
21 - MAR - 2000; 2000US-191048P.
21 - MAR - 2000; 2000US-191048P.
21 - MAR - 2000; 2000US-193032P.
29 - MAR - 2000; 2000US-193032P.
29 - MAR - 2000; 2000US-193032P.
29 - MAR - 2000; 2000US-194449P.
40 - APR - 2000; 2000US-194647P.
11 - APR - 2000; 2000US-196690P.
11 - APR - 2000; 2000US-196820P.
11 - APR - 2000; 2000US-196820P.
11 - APR - 2000; 2000US-19858P.
25 - APR - 2000; 2000US-19550P.
25 - APR - 2000; 2000US-19550P.
25 - APR - 2000; 2000US-19550P.
25 - APR - 2000; 2000US-19554P.
03 - MAY - 2000; 2000US-19554P.
03 - MAY - 2000; 2000WS-US14941.
02 - UN-2000; 2000WS-US14988.
24 - AUG-2000; 2000WS-US34956.
08 - NOV-2000S-200WS-US33678.
08 - NOV-2000S-200WS-US33678.
09 - DEC-2000; 2000WS-US34956.

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J, Smith V,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids encoding PRO polypeptides, used to diagnose the nce of tumours, such as prostate and breast tumours, in mammals and reen for modulators of the compounds -
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                                                                                            TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACACTCCACTCTACCAATGAAGTGA
                                                                                                      TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
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98.6%;
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07-CCT-1998;
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19-MAR-2000;
24-FEB-2000;
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26-JUN-2000;
27-MAY-2000;
28-JUN-2000;
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20-DEC-2000;
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2000WO-US0504
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factor alpha release; chondrocyte cell; proliferation;
tumour; gene therapy; ss.
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Qy 240 AGGTTAAAAATGCCCAGCTGGCAGGGGGCCAAAGGAGTCATTCTCTAGTCAGACCCTGCTG 299	Query Match 84.7%; Score 1687.2; DB 25; Length 2558; Best Local Similarity 98.6%; Pred. No. 0; Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;	10-SEP-1998; 10-SEP-1998; 10-SEP-1998; 10-SEP-1998;	02-SEP-1998; 02-SEP-1998; 02-SEP-1998; 09-SEP-1998;	26-AUG-1998; 26-AUG-1998; 26-AUG-1998; 01-SEP-1998;	26-AUG-1998; 26-AUG-1998; 26-AUG-1998; 26-AUG-1998;	17-AUG-1998; 18-AUG-1998; 18-AUG-1998; 18-AUG-1998;	17-AUG-1998; 17-AUG-1998; 17-AUG-1998; 17-AUG-1998;	24-JUL-1998; 04-AUG-1998; 10-AUG-1998; 10-AUG-1998;	02-JUL-1998; 02-JUL-1998; 02-JUL-1998; 02-JUL-1998;	26-JUN-1998; 01-JUL-1998; 01-JUL-1998; 01-JUL-1998;	25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 26-JUN-1998; 26-JUN-1998;	25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 25-JUN-1998;	24-JUN-1998; 24-JUN-1998; 24-JUN-1998; 24-JUN-1998;	22-JUN-1998; 24-JUN-1998; 24-JUN-1998; 24-JUN-1998;	18-JUN-1998; 19-JUN-1998; 22-JUN-1998; 22-JUN-1998;	16-JUN-1998; 17-JUN-1998; 17-JUN-1998; 17-JUN-1998;	PR 11-JUN-1998; 98US-088863P. PR 11-JUN-1998; 98US-088876P. PR 12-JUN-1998; 98US-089090P. PR 12-JUN-1998; 98US-089105P. PR 12-JUN-1998; 98US-089105P.
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ALTONMENT

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RESULT 1
FOH1_HUMAN
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Q04609; Q04748; Q1305; Q9NP15; Q9NYE2; Q9P1P8;

Q1-JUN-1994 (Rel. 29, Created)

Q1-JUN-1994 (Rel. 29, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Glutamate carboxypeptidase II (EC 3.4.17.21) (Membrane glutamate carboxypeptidase) (mGCP) (N-acetylated-alpha-linked acidic dipeptidase I) (NALADase I) (Pteroylpoly-gamma-glutamate carboxypeptidase)

[FOLYlpoly-gamma-glutamate carboxypeptidase)
                                                                                                 SEQUENCE FROM N.A. (ISOFORM PSMA-1).

SEQUENCE FROM N.A. (ISOFORM PSMA-1).

MEDLINB-99057588; PubMed-9838072;

O'Keefe D.S., Su S.L., Bacich D.J., Horiguchi Y., Luo Y., Powell C.T., Zandvilet D., Russell P.J., Molloy P.L., Nowak N.J., Shows T.B., Mullins C., Vonder Haar R.A., Fair W.R., Heston W.D.W.;

"Mapping, genomic organization and promoter analysis of the human prostate-specific membrane antigen gene.";

Biochim. Biophys. Acta 1443:113-127(1998).
TEQUENCE FROM N.A. (ISOFORM PSMA-1).
TISSUE-Brain;
MEDLINE-993620085; PubMed-9694964;
Luthi-Carter R., Barczak A.K., Speno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95188188; PubMed=7882349; Su S.L., Huang I.-P., Fair W.R., Powell C.T., Heston W.D.W.; Su S.L., Huang Il-P., Fair W.R., Powell C.T., Heston W.D.W.; "Alternatively spliced variants of prostate-specific membrane antigen RNA: ratio of expression as a potential measurement of progression."; Cancer Res. 55:1441-1443(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Israeli R.S., Powell C.T., Fair W.R., "Molecular cloning of a complementary membrane antigen.", Cancer Res. 53:227-230(1993).
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98041505; PubMed=9375657;
Bzdega T., Turi T., Wroblewska B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Prostatic carcinoma; MEDLINE=93113576; PubMed=8417812;
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                                                                                                                                                                                                                                                                                                "Molecular cloning of a peptidase against N-acetylaspartylglutamate from a rat hippocampal cDNA library.";
J. Neurochem. 69:2270-2277(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue=Prostate;
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Speno H.S., Luthi-Carter R., Macias W.L. Joshi A.R.T., Coyle J.T., "Site-directed mutagenesis of predicted glutamate carboxypeptidase II."; Mol. Pharmacol. 55:179-185(1999).
                                                                                                                                                                                                     Rawlings N.D., Barrett A.J.;
"Structure of membrane glutamate carboxypeptidase.";
Biochim. Biophys. Acta 1339:247-252(1997).
                                                                                                                                MEDLINE-99102317; PubMed-9882712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              against N-acetylaspartylglutamate (NAAG) from human and systems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTITAL SEQUENCE FROM N.A. (ISOFORMS PSMA-3 AND PSMA-4).

LUDOLD S.E., Criley S.C., Coffers the prostate specific membrane antigen.";

"Alternative Splicing of the prostate specific membrane antigen.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                MUTAGENESIS
                                                                                                                                                                                                                                                                                     DOMAIN STRUCTURE.
MEDLINE=97330810; PubMed=9187245;
                                                                                                                                                                                                                                                                                                                                                                   Luthi-Carter R., Barczak A.K., Speno H.D., Coyle J.T.; "Hydrolysis of the neuropeptide N-acetylaspartylglutamate (NAAG) cloned human glutamate carboxypeptidase II."; Brain Res. 795:341-348(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE=98288196; PubMed=9622670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate-specific membrane antigen
carcinoma cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Prostatic carcinoma;
MEDLINE-99025849; PubMed-9809977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Glutamate carboxypeptidase II: a polymorphism associated with lower levels of serum folate and hyperhomocysteinemia."; hum. Mol. Genet. 9:2837-2844(2000).
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Smith A.D., Halsted C.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20545101; PubMed=11092759;
Devlin A.M., Ling E.-H., Peerson J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl peptidase IV activity.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular characterization of human brain N-acetylated alpha-linked acidic dipeptidase (NAALADase).";
J. Pharmacol. Exp. Ther. 286:1020-1025(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grauer L.S., Lawler K.D., Marignac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 60-74, AND SUBCELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holt G., Ferrer K.T., Heller M.,
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                                                                                                        W.L.,
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FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-acidic dipeptidase (NAALADase) activity. Has a preference for trial-alpha-glutamate peptides. In the intestine, required for the uptake of folate. In the brain, modulates excitatory neurotransmission through the hydrolysis of the neuropeptide, N-aceylaspartylglutamate (NAAG), thereby releasing glutamate. Stable at pH greater than 6.5. Isoforms PSM-4 and PSM-5 would appear to be physiologically irrelevant. Involved in prostate tumor
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progression.
-!- FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity.
-!- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
-!- COFACTOR: Zinc; Binds two ions per subunit. Required for NAALADase

NAAG, quisqualic acid, 2-(phosphonomethyl) penti (PMPA) and EDTA. Activated by cobalt. SUBCELLULAR LOCATION: Type II membrane protein. The PSMA' isoform is cytoplasmic. ENZYME REGULATION: The NAALADase activity activity 2-(phosphonomethyl) pentanedioic S. inhibited by beta-

Plasma membrane

ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=6; Comment-Experimental confirmation may isotorms bе lacking for

Name=PSMA-Name=PSMA-1; IsoId=Q04609-1; Sequence=Displayed

IsoId=Q04609-2; Sequence=VSP_005341

Name=PSMA-4 Name=PSMA-3 IsoId=Q04609-3; Sequence=VSP_005342,

Name-PSMA-5 IsoId=Q04609-4; IsoId=Q04609-5; Sequence=VSP_005337, Sequence=VSP_005339, VSP_005340; VSP_005338

Name=PSMA IsoId=Q04609-6; Sequence=VSP_005336;

Expressed specifically in jejunum brush border membranes. In the brain, highly expressed in the ventral striatum and brain stem. If the prostate, the PSMA, cytosolic isoform is the most abundant form in normal tissue, the membrane-bound PSMA-1 form in primary prostate tumors. The PSMA-2 isoform also found in normal prostate as well as in brain and liver.

INDUCTION: In the prostate, up-regulated in response to androgen colon and the capillary endothelium of a variety of tunors. Expressed specifically in jejunum brush border membranes. expressed, TISSUE SPECIFICITY: CIFICITY: Highly expressed in prostate epithelium. in the small intestine, brain, kidney, liver, spl spleen, prostate Also

cardiovascular disease, neural tube defects,

MISCELLANEOUS: PSMA is used as a diagnostic and prognostic indicator of prostate cancer, and as a possible marker for neurological disorders such as schizophrenia, Alzheimer's of the control of the con disease various

and Huntington's disease.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.

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EMBL; M99487; AA EMBL; S76978; AA EMBL; AF007544; ; AAA60209.1; -. ; AAB33750.2; -. 44; AAC83972.1; -

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077564;
28-FEB-2003
                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamate carboxypeptidase II (EC 3.4.17.21) (Membrane glutamate
carboxypeptidase) (MGCP) (N-acetylated-alpha-linked acidic dipeptidase
carboxypeptidase I) (Pteroylpoly-gamma-glutamate carboxypeptidase)
(FOLY-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase
(FOLY-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase
) (Prostate-specific membrane antigen homolog).
                                                Halsted C.H., Gardner J.M.,
              CHARACTERIZATION
                                                                                                                         Molecular
                                                                                                                                              Halsted C.H., Ling E.-H., Luthi-Carter Gardner J.M., Coyle J.T.;
                                                                                                                                                                                              SEQUENCE FROM N.A.,
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                           Sus scrota (Pig)
 MEDLINE-86085936;
                                                                                                                                                                      TISSUE-Jejunal mucosa;
MEDLINE-98352082; PubMed-9685395;
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                                                                                                                                                                                                                                                                       FOLH1 OR NAALAD1
                                                                                                                                   "Folylpoly-gamma-glutamate
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                                 Ling E.-H., Luthi-Cart
Coyle J.T.;
. 275:30746-30746(2000)
                                                                                                273:20417-20424(1998)
                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
 PubMed=2867095;
                                                                                                                                                                                              AND
                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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98.0%;
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and relation to o
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Pfam; PF02225; PA; 11.
Pfam; PF04389; Peptidase_M28;
Pfam; PF04253; TFR_dimer; 1.
Hydrolase; Carboxypeptidase; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purification and characterization.";
J. Biol. Chem. 261:928-933(1986).
-!- FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-
                                                                                                                                                                           METAL
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chandler C
                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF050502; AAC39269.1; MEROPS; M28.010; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>:</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Pteroylpolyglutamate hydrolase
                                                                                     CARBOHYD
                                                                                                   CARBOHYD
                                                                                                              CARBOHYD
                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         excitatory neurotransmission through the hydrolysis of the neuropeptide, N-aceylaspartylglutamate (NAAG), thereby releasing glutamate. Maximal activity at pH 6.0. FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity (By similarity). In vitro, cleaves Gly-Pro-AMC (By similarity). CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jejunum brush-border membrane. Weak expression DOMAIN: The NAALADase activity is found in the dipeptidyl peptidase IV type activity in the C-SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glutamyl residue COFACTOR: Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (By similarity).
TISSUE SPECIFICITY: High expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity by 50%.
SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acidic dipeptidase (NAALADase) activity. Has a preference alpha-glutamate peptides (By similarity). In the intestine required for the uptake of folate. In the brain, modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME REGULATION: The NAAI quisqualic acid, beta-NAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PMPA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .J., Wang
           388
426
454
554
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275
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629
667
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                                                                                                                                                                                                                                                                                                                                                         Serine
                                                                                                                                                                                                                                                                                                                                            Multifunctional enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATION: The NAALADase activity is inhibited by cid, beta-NAAG and 2-(phosphonomethyl) pentanedioic Ethanol ingestion decreases the folate hydrolase
             т.т.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binds two ions per subunit. Required
                                                                                                                                                                                                                                                                                                                                                         protease; Transmembrane;
                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halsted
                                                                                                                                              NUCLEOPHILE (NAALADASE) (BY SIN CHARGE RELAY SYSTEM (POTENTIAL) CHARGE RELAY (POTENTIAL) CHARGE RELAY (POTENTIAL)
                   N-LINKED (GLCNAC.
                                                                                                                                    CHARGE RIZINC 2 (1 ZINC 1 Ar ZINC 1 (F ZINC 1 (F ZINC 2 (F ZINC 1 (F N-LINKED
                                                                                                                                                                                                                                                                                                                                                                     Metalloprotease;
                                                                                                                                                                                                                                                                 POLY-PRO.
NAALADASE.
                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                  SIGNAL-ANCHOR
                                                                                                                          N-LINKED
                                                                                                                                                                                                                                                                                            EXTRACELLULAR
                                                                                                                                                                                                                                                                                                        POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                              from
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                                                                                                                                    (GLCNAC. .
                                                                                                                          (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the duodenum
                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
OR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jejunal brush borders.
                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                         Glycoprotein,
                                                                                                                                                                                                                                                                                                                                                                     Zinc; Aminopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-terminal.
                                                                                                                                                                                                                             (POTENTIAL)
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central
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(POTENTIAL).
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-ral region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intestine,
                                                                                                                                                                                                                                                    (BY SIMILARITY).
           POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for NAALADase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration
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AA;

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CRC64;

Query Match Best Local 9

Matches

397;

Conservative

21;

Mismatches

Similarity

91.3%;

Score 2126; Pred. No. 2.

DB 1; 2.9e-150;

DB

Length 751; Indels

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RESULT 3
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glutamate carboxypeptidase II (EC 3-4.17.21) (Membrane glutamate carboxypeptidase) (mGCP) (N-acetylated-alpha-linked acidic dipeptidase II) (RAALADase I) (Ptercylpoly-gamma-glutamate carboxypeptidase)
(FOlylpoly-gamma-glutamate carboxypeptidase)
(FOlylpoly-gamma-glutamate carboxypeptidase)
                       MEDLINE=98169524; PubMed=9501243; Luthi-Carter R., Berger U.V., Barczak A.K., "Isolation and expression of a rat brain cDt carboxypeptidase II."; Proc. Natl. Acad Cart.
                                                                                                                                                                                                                                            "Molecular cloning of a peptidase agai
from a rat hippocampal cDNA library.";
J. Neurochem. 69:2270-2277(1997).
                                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague-Dawley: TISSUE-Hippocampus;
MEDLINE-98041505; PubMed-9375657;
Bzdega T., Turi T., Wroblewska B., She D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                         peptidase against N-acetylaspartylglutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Ver
Sciurognathi;
                            95:3215-3220(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                She D., Chung H.S., Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                   cDNA encoding
                                                                                                             Enna M.,
                                                                                Coyle J.T.;
ng glutamate
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Name=3; Synonyms=Long form;
IsoId=P70627-3; Sequence=Not described;
IsoId=P70627-3; Sequence of the hippocampus, dentate gyrus, priform cortex, choroid plexus of venticles, pineal gland, anterior lobe of the pituitary gland and supraoptic nucleus. High levels also found in the cerebral cortex, substantia nigra, pontine nucleus and the granule cell layer of cerebellum. Highly expressed in astrocytes and non-myelinating Schwann cells. Also expressed in kidney, localizing to the proximal brush border of the renal tube.

-i- DOMAIN: The NAALADase activity is found in the central region, the dipeptidyl peptidase IV type activity in the C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96149377; pubMed-8570628;
Carter R.E., Feldman A.R., Coyle J.T.;
"Prostate-specific membrane antigen is a hydrolase w
pharmacologic characteristics of a neuropeptidase.";
Proc. Natl. Acad. Sci. U.S.A. 93:749-753(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity (By similarity). In vitro, cleaves Gly-Pro-AMC (By similarity).
-!- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE SPLICING.
Bzdega T., She D., Turi T., Wroblewska B., Neale J.H.;
"Molecular cloning of alternatively spliced variants of
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luthi-Carter R., Berger U.V., Barczak A.K., Enna M., Co
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 284-752 TISSUE=Brain;
                                                                                                                                                                     entities
                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 284-752 FROM N.A.
                                                                                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-acidic dipeptidase (NAALADase) activity. Has a preference for trialpha-glutamate peptides (By similarity). In the intestine, required for the uptake of folate. In the brain, modulates excitatory neurotransmission through the hydrolysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME REGULATION: The NAALADase activity is inhibited by beta-
NAAG, quisqualic acid and 2-(phosphonomethyl)glutaric acid (PMG
SUBCELLULAR LOCATION: Type II membrane protein. Plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glutamyl residue,
COFACTOR: Zinc; B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuropeptide, N-aceylaspartylglutamate (NAAG),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity)
AF040256;
AF039707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P70627-1; Sequence=Displayed
ame=2; Synonyms=Short form;
IsoId=P70627-2; Sequence=Not descri
                                                                      U75973; AAC53423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note=Probably inactive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoforms;
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                                                                                                                                     an
                                                                                                                                     requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurosci.
   AAB96759.1;
                                      AAC40067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 described;
                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                 There are no rest
                                                                                                                                                                                                                   Usage
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MEROPS; M28.010;

IPR003137; PA. 225; PA; 1.

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RESULT 4
FOH1_MOUSE STANDARD;
AC 035409; Q9DCC2;
DT 28-FEB-2003 (Rel. 41, Created)
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Dipeptidase; Serine protease; Transmembrane; Glycoprotein;
Signal-anchor; Multifunctional enzyme; Alternative splicing
DOMAIN

1 19 CYTOPLASMIC (FOTENTIAL).
TRANSMEM 20 44 SIGNAL-ANCHOR (TYPE-II MEMBRAN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
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87.1%;
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ZINC 1 (BY SIMILARITY) CHARCE (GLUAG. . .) (POTEN) CHARCE (GL
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Pred. No. 8
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EXTRACELLULAR (POTENTIAL).
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RAGE RELAY SYSTEM (POTENTIAL)
CC 1 (BY SIMILARITY).
CC 1 AND 2 (BY SIMILARITY).
CC 1 (BY SIMILARITY).
CC 1 (BY SIMILARITY).
CC 1 (BY SIMILARITY).
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8.4e-146;
hes 28;
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( POTENTIAL).
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RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
Ra Sanaki H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamate carboxypeptidase II (EC 3.4.17.21) (Membrane glutamate carboxypeptidase) (mGCP) (N-acetylated-alpha-linked acidic dipeptidase I) (NALADase I) (Pteroylpoly-gamma-glutamate carboxypeptidase)
(FOLYpoly-gamma-glutamate carboxypeptidase)
(FGCP) (Folate hydrolase
I) (Prostate-specific membrane antigen homolog).
FOLH1 OR MOPSM OR NAALAD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-NIH SWISS; TISSUE-Brain;
STRAIN-NIH SWISS; TISSUE-Brain;
MEDLINE-21077522; PubMed-11210180;
MEDLINE-21077522; PubMed-11210180;
MEDLINE-21077522; PubMed-1120180;
Heston W.D.W.;
"Cloning, expression, genomic localization, and enzymatic activities
"Cloning, expression, genomic localization, and enzymatic activities
of the mouse homolog of prostate-specific membrane antigen/NAALADase/
folate hydrolase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TMEDLINE=21085660;
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          TISSUE SPECIFICITY: Expressed predominantly in the hippocampal region of the brain and in kidney. Lower levels in the ovary, testis and mandibular gland.

DOMAIN: The NAALADase activity is found in the central region, dipeptidyl peptidase IV type activity in the C-terminal.

SIMILARITY: BELONGS TO PETIDASE FAMILY M2BM.

CAUTION: There are amino acid differences between the sequence shown in fig.1 (Ref.1) and the sequence deposited in the databb (AF026380). The sequence from fig.1 shows only 3 conflicts between 1 and Ref.2. These are at AA positions 141, 240 and 287.
                                                                                                                                                                                                                                  activity.

activity.

ENZYME REGULATION: The NAALADase and are inhibited by quisqualic acid.

Type II membran
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                                                                                                                                                                                                                      similarity).
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; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                         membrane
                                                                                                                                                                                                                                                                                 folate
                                                                                                                                                                                                                                         protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-acetylated-alpha-linked-
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                                                                                                                                                                                                                                                                               hydrolase activities
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; Murinae; Mus
                                                                                                                                                                                                                                         Plasma
                                                                                                                                                                                                                                           membrane
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METAL
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GO:0005887; C:integral to plasma membrane; IDA.
GO:0008464; F:gamma-glutamyl hydrolase activity; IDA.
GO:0004237; F:membrane dipeptidase activity; IDA.
GO:0004760; P:folic acid and derivative metabolism; IDA.
erpro; IPR003137; PA.
m; PF02225; PA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF04389; Peptidase_M28; PF04253; TFR_dimer; 1.
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                                                                            EGKSLYDSWKEKSPSPEFIGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWKTNKVSS
                                                                                                                                                                                                                                                            LGSTEWAEEHSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELQSPDEGF
                                                                                                                                                                                                                                                                                    LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
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DKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMNDQL
                                                                                                                                                                               EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSG
                                                  YPLYHSVYETYELVVKFYDPTFKYHLTVAQVRRAMVFELANSIVLPFDCQSYAVALKKYA
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Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
N-acetylated-alpha-linked acidic dipeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99185063; PubMed=10085079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                            Genew; HGNC:14526; NAALAD2.

G0; G0:0016021; C:integral to membrane; NAS.

G0; G0:0004180; F:carboxypeptidase activity; NAS.

G0; G0:0004274; F:dipeptidyl-peptidase IV activity;

G0; G0:0004274; F:dipeptidyl-peptidase IV activity;

G0; G0:0005508; P:proteolysis and peptidolysis; NAS.

InterPro; IPR003137; PA.
                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol.
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                                                                                                                                               EMBL; AJ012370; CAB39967.1; -.
                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                           between
                                                                                                                                      MEROPS; M28.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 274.8470-8483(1999).

Biol. Chem. 274.8470-8483(1999).

FUNCTION: Has N-acetylated-alpha-linked-acidic dipeptidase runchabase) activity. Also exhibits a dipeptidyl-peptidase (NAALADase) activity. In vitro, cleaves Gly-Pro-AMC.

CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal Chem. Catalylically from Ac-Asp-Glu or pteroyl-gamm glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamm
                                                                                                                                                                                                                                                                                                    putamen and superior colliculus.

DOMAIN: The NAALADase activity is found in the dipeptidyl peptidase IV type activity in the SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type II membrane protein (Potential). TISSUE SPECIFICITY: Highest expression in the testis. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR: Zinc; Binds two ions per
                                                                                                                                                                                                                                                                                                                                                             in ovary and spleen. Weak expression in prostate, heart placenta. In brain, expressed in striatum, parietal corventral striatum with lower levels in hippocampus, brain
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OSCZE2;
OSCZE2;
28-FEB-2003 (Rel. 41, Createu,
28-FEB-2003 (Rel. 41, Last sequence
P 28-FEB-2003 (Rel. 41, Last annotation
N-acetylated-alpha-linked acidic di
NAALADase II) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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SEQUENCE
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Hydrolase; Carboxypeptidase; Metalloprotease;
                                                                                    NLD2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                599
                                                                                                                                         719
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                                                                                                                                                                                                          361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                          DRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKBGWRPRRTILFASWDAEEFGL
                                                                                                                                                                                                                              ASIYNLSKKHDQQLTDHGVSFDSLFSAVKNFSEAASDFHKRLIQVDLNNPIAVRMMNDQL
                                                                                                                                                                                                                                           DKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMNDQL
                                                                                                                                                                                                                                                                                                                               EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWEINKFSG
                                                                                                                                                                                                                                                                                                                                                                            LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP
                                                                                                                                         KKHISIAAFTIQAAAGTLKEV
                                                                                                                                                     KRQISVAAFTVQAAAETLSEV
                                                                                                                                                                                   MFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDV
                                                                                                                                                                                                                                                                                                                                                                                                             DRYVILGGHRDSWVFGAIDPTSGVAVLQEIARSFGKLMSKGWRPRRTIIFASWDAEEFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGGIAPPDKSWKGALNVSYSIGPGFTGSDSFRKVRMHVYNINKITRIYNVVGTIRGSVEP
                                                                                                                                                                                                                                                                                                                      ESKSLYESWLEKDPSPENKNLPRINKLGSGSDFEAYFQRLGIASGRARYTKNKKTDKYSS
                                                                                                                                                                                                                                                                                                                                                                 LGSTEWAEENVKILQERSIAYINSDSSIEGNYTLRVDCTPLLYQLVYKLTKEIPSPDDGF
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264
414
618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑĄ,
                                                                                    STANDARD;
                  1, Created)
1, Last sequence update)
11, Last annotation update)
11, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         740
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ZINC 1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED
N-LINKED
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ZINC 1 (B
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N-LINKED
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
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                                                                                                                                         739
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                              (
편
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 740;
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                              3.4.17.
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh J.,
RA Gustincich S., Hill D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shlbata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wilming L.,
RA Hysashizaki Y.,
Ra Hayashizaki Y.,
                             Query Match
Best Local
     Matches
                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for corentitles requires a license agreement (See http://www.isb-sib.ch/acressend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).

-!- FUNCTION: Has N-acetylated-alpha-linked-acidic dipeptidase (NAALADase) activity (By similarity). Also exhibits a dipeptidyl-peptidase IV type activity. In vitro, cleaves Gly-Pro-AMC (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Carboxypeptidase; Metalloprotease; Dipeptidase; Serine protease; Transmembrane; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF04389; Peptidase_M28;
Pfam; PF04253; TFR_dimer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; M28.012; -. MGD; MGI:1919810; Naalad2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK012270; BAB28132.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma. COPACTOR: Zinc; Binds two ions per subunit. Required for NAALADase activity (By similarity).

SUBCELLULAR LOCATION: Type II membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: The NAALADase activity is found in th dipeptidyl peptidase IV type activity in the SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
al Similarity
167; Conserv
                                                                                                                  1
135
173
196
60
120
145
257 i
     Conservative
                                                                                                                                                                                                                                                                                                                                                                     Serine protease; Tr; Multifunctional
                                                                                                                     A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11217851;
                                                                                                                                               94
135
173
196
196
120
                                39.3%;
                                                                                                                     MW;
                                                                                                               CHARGE RELAY SYSTEM (POTEN)
CHARGE RELAY SYSTEM (POTEN)
CHARGE RELAY SYSTEM (POTEN)
ZINC 1 (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTEN)
N-LINKED (GLCNAC...) (POTEN)
N-LINKED (GLCNAC...) (POTEN)
  Pred. No. 5.20
3; Mismatches
                                Score 916;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                 NAALADASE.
                                                                                                                                                                                                                                                                                                                                                                        enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                             Zinc; Aminopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the central r
ne C-terminal.
                                                       Length 257;
                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
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191 KKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLDL_RAT 054697;
                                                                                                                                                                                                                                    This SWI
between
                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-acetylated-alpha-linked acidic dipeptidase like protein (EC 3.4.17.21) (NAALADase L) (Ileal dipeptidylpeptidase) (100 ileum brush border membrane protein) (I100).
 Dipeptidase; S
Signal-anchor;
                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shneider B.L., Thevananther S., Moyer M.S., Walters H.C., Devarajan P., Sun A.Q., Dawson P.A., Ananthanarayanan M.; "Cloning and characterization of a novel peptidase from ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley; TISSUE-Ileum; MEDLINE-98049571; PubMed-9388249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                              Hydrolase; Carboxypeptidase; Metalloprotease;
                                               Pfam;
                                                                                              InterPro;
                                                                                                         MEROPS; M28.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ileum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol.
                                                                                                                                                                                                                                                                                                                                          Cleaves Gly-Pro-AMC.

CAPALITIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or ptercyl-gamma. COFACTOR: Zinc; Binds two ions per subunit (By similarity). SUBCELLULAR LOCATION: Type II membrane protein. Ileal brush b
                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                  intestine.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: Mainly expressed in the distal small
                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Has no NAAG hydrolyzing activity (By similarity). Exhibits a dipeptidyl-peptidase IV type activity. In vitro,
                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                               PF04389; Peptidase_M28; PF04253; TFR_dimer; 1.
                                                                                                                            AF009921; AAB87644.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                            PF02225; PA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chem.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
N-acetylated alpha-linked acidic dipeptidase like
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brush border membrane protein) (1100)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pangalos M.N., Neefs J.-M., Somers M., Verhasselt P., Bekkers M., van der Helm L., Fraiponts E., Ashton D., Gordon R.D.; "Isolation and expression of novel human glutamate carboxypeptidases"
                                                                                                                  EMBL; AJ012371; CAB39968.1; EMBL; AF010141; AAB87645.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shneider B.L., Thevananther S., Moyer M.S., Walters H.C., Rinaldo Devarajan P., Sun A.Q., Dawson P.A., Ananthanarayanan M.; "Cloning and characterization of a novel peptidase from rat and h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl peptidase IV activity.";
J. Biol. Chem. 274:8470-8483(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Small intestine;
MEDLINE=99185063; PubMed=10085079;
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                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Mainly expressed in the distal small intestine. Also expressed in the spleen and testis. Weak expression in the brain, locating mainly to the brain sto amygdala, thalamus and ventral striatum. Isoforms 2 and found in the small intestine and colon
                                                                                                                                                                                                                                                                                                                                                                   found in the small intestine and colon. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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PF04389; Peptidase_M28; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
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METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Aminopeptidase; Dipeptidase; Serine protease; Transmembrane; Glycoprotein; Signal-anchor; Multifunctional enzyme; Alternative splicing.

DOMAIN

CYTOPLASMIC (POTENTIAL).

TRANSMEM

7

28

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF04253; TFR_dimer; 1.
                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                               298
                                                                                                                                                            185;
                                                                                        58
                                                                                                                                                                     Similarity
                                                                                                               LNGTLAP-ATWQGALGCHYRLGPGFRPDGDFPADSQVNVSVYNRLELRNSSNVLGIIRGA
DEGFEGKSLYESWTK--KSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWE
                                                                                                                                 MGGSAPPDSSWRGSLKVSYNVGPGF--TGNF-STQKVKMHIHSTNEVTRIYNVIGTLRGA 57
                                 EFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSP 176
                                                                                        VEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEG-WRPRRTILFASWDAE 116
                      EFGL1GSTEFTEEFFNKLQERTVAY I NVD1SVFANATLRVQGTPPVQSVVFSATKE1RSP
                                                                   VEPDRYVLYGNHRDSWVHGAVDPSSGTAVLLELSRVLGTLLKKGTWRPRRSIVFASWGAE
                                                                                                                                                                                                   420
740
                                                                                                                                                                                                                                        636
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                                                                                                                                                                                                                                                                                               580
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                                                                                                                                                                                                                                                                                                                                                                                                    502
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                                                                                                                                                                                                       AA;
                                                                                                                                                                                                    424 I
80620 MW;
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                                                                                                                                                                    37.1%;
                                                                                                                                                            91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM (PÓTÉNTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
ZINC 2 (BY SIMILARITY).
ZINC 1 AND 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
                                                                                                                                                                                                   Missing (in isoform 8
/FTId=VSP_005353.
LIGST -> SPGLO (IN RE
E2E5AAC9E5056A14 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
Missing (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                        Pred. No. 1.7e
1; Mismatches
                                                                                                                                                                   Score 863.5; D
Pred. No. 1.7e-
                                                                                                                                                                                                                                                                                  Missing (in isoform 7).
/FTId=VSP_005351.
                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform 5). /FTIG=VSP_005347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_005345.
PSLGSLGAGSDYAPFVHFLGI ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing (in isoform 3).
                                                                                                                                                                                                                                                (in isoform 8).
/FTId=VSP_005352
                                                                                                                                                                                                                                                                         GPLVTAVEKFEAEAAAL
                                                                                                                                                                                                                                                                                                                               FSSHQAVARTAGSVILRL
                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform 6).
                                                                                                                                                                                                                                                                                                                                                                            PGQRGV (in isoform 6).
                                                                                                                                                                                                                                                                                                                                                                                                   PSLGSLGAGSDYAPFVHFLGISSMDIAYTYDRSKTSARIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                               DSPAQ (in isoform 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHLSLSSGSLPLFLWP (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_005344.
P -> PGEPSSCCLHPRPLLCSGCRCPHPALPLPPPSPAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOPHILE (NAALADASE) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VSP_005343
                                                                                                                                                                                                                                                                                                         /FTId=VSP_005350
                                                                                                                                                                                                                                                                                                                     (in isoform 7
                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP_005346
                                                                                                                                                                                                                                                                                                                                                                                       -> PRARLOPGSPPTTQPLTPLTMWTSFWTRASAAIRLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _005348
                                                                                                                                                                                                                                                                                                                                            _005349
                                                                                                                                                                                  DB
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-56;
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1 CRC64;
                                                                                                                                                                                                                                                                                                                                 -> FEEGDKGHPETRTGEAED
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                                                                                                                                                            Indels
                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                         GMHSPDPEVWGALHPHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRLQQPSGCGPDSGEC
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                                                                                                                                                            39;
                                                                                                               356
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RESULT 9
GCP2_CAEEL
ID GCP2_C.
AC P91406
DT 28-FEB
DE Glutam
GN R57.1.
OS Caenor
OC Rhabdil
OX NCBI_T
RN [1]
RR SEQUEN
RA SEQUEN
RA Favell
RA SUBMIT
CC -1- CO
CC -1- 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
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      ACT_SITE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003
28-FEB-2003
Glutamate ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Favello A., Rifkin L., Chiapelli B.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.

- COFACTOR: Zinc; Binds two ions per subunit (By similarity).

- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003137; PA.
Pfam; PF02225; PA; 1.
Pfam; PF04389; Peptidase_M28; 1.
Pfam; PF04253; TFR_dimer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; M28.010; -.
WormPep; R57.1; CE12844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U88179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P91406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCP2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-FEB-2003 (Rel. 41, Last annotation update) utamate carboxypeptidase II homolog (EC 3.4.17.21).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T30154;
                                                                                                                                                                                                                                                                                             hetical protein; Hydrolase; Carboxypeptidase; Metalloprotease; Transmembrane; Glycoprotein; Signal-anchor.
N 1 6 CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NACSRARDTASGSEAWAEVQRQLSIVVTALEGAAATLRPVA 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DALFDIESKYDPSKAWGDVKRQISVAAFTVQAAAETLSEVA 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSPDPLQVRMLNDQLMLLERTFLNPRAFPEERYYSHVLWAPSHGLRSH-----IPGLS
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
         24
263
416
368
378
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543
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578
416
368
378
417
445
543
                                                                                                                                                                                                                                                                    e; Glycoprotein;
6 CYTOPL
23 SIGNAL
EXTRACELLULAR (POTENTIAL).
CATALYTIC (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II
                                                                                                                                                                                                                                            (POTENTIAL).
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                                                                                                                                                                                                                                                                       PROTEIN)
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RESULT 10
GCP2_ARATH
ID GCP2_ARATH
ID GCP2_ARATH
ID GCP2_BRATH
ID GCP2_BRATH
ID GCP2_BRATH
ID GCP2_BRATH
ID GCP2_BRATH
ID 28-FEB
DT 28-F
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AMP1 OR AT3G54720 OR T5N23_80.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids_II_ Brassicales; Brassicaceae; Arabidopsis.
                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable glutamate carboxypeptidase II (EC 3.4.17.21).
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBI_TaxID=3702; [1]
SEQUENCE FROM N.A.
STRAIN=CV. Landsberg erecta; TISSUE=Siliques; MEDLINE=21434423; PubMed=11549767:
Helliwell C.A., Chin-Atkins A.N., Wilson I.W., Chapple R., Dennis E.S., Chaudhury A.; "The Arabidopsis AMP1 gene encodes a putative glutamate carboxypeptidase."; Plant Cell 13:2115-2125(2001). [2]
SEQUENCE FROM N.A.
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RA De Simone V. Choisne N. Artiquenave F. Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Surin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Fuchs M., Benes V.,
RA Wincker P., Collado C., Peret P., Kolland R., Brandt P., Nyakatura G.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Rooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Malti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feilblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Muraki A.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT. Mathro A., Plant A., Analysis of chromosome 3 of the plant Arabidopsis
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PIR; T47631; T47631
                                                                                                                                                                                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                  InterPro; IPR003137; PA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: May modulate the level of one or more small signaling molecules that have a role in regulating meristem function. CATMALYTIC ACTIVITY: Release of an unsubstituted, C-terminal glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma. COFACTOR: Zinc; Binds two lons per subunit (By similarity). SUBCELLULAR LOCATION: Type II membrane protein. TISSUE SPECIFICITY: Expressed in all plant parts. Highest levels in the bolt stem, inflorescence, root and silique. Low level in
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYCD3 expression.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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PF04389; Peptidase_M28;
PF04253; TFR_dimer; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                           Carboxypeptidase; Metalloprotease; Zinc; Transmembrane; in; Signal-anchor.
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(POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CATALYTIC.

NUCLEOPHILE (BY SIMILARITY).

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ZINC 1 (BY SIMILARITY).
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ZINC 1 (BY SIMILARITY).

N-LINKED (GLCNAC. ...) (PO

E -> K (IN MUTANT STRAIN P

MISSING (IN REF. 2).

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JAN...
TOPUTES: 075422; Q9HA99; Q9NAV...
1 Q9UTES: 075422; Q9HA99; Q9NAV...
T 28-FEB-2003 (Rel. 41, Created)
T 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
T-mansferrin receptor protein 2 (TfR2).
                     Manual H., Yang K., ...
Kawabata H., Yang K., ...
Koeffler H.P.;
Koeffler H.P.;
"Molecular cloning of transferrin receptor transferrin receptor-like family.";
transferrin receptor-like family.";
reiol. Chem. 274:20826-20832(1999).
SEQUENCE FROM N.A. MEDLINE=99018118; !
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                  TISSUE=Erythroleukemia, and Myeloid MEDLINE=99340005; PubMed=10409623;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
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  PubMed=9799793;
                                                                                                                                                                                                         (ISOFORMS ALPHA AND
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Primates; Catarrhini; Hominidae;
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Schattevoy R., Boright A.P., Weber J.,

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SEQUENCE OF 1-150 AND SEQUENCE OF 1-150 AND EMBRYO;
TISSUB-Carcinoma, and Embryo;
TISSUB-Carcinoma, and Embryo;
Isogai T., Ots T., Hayashi K., Sugana T., Otsuki T., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Takiguchi S.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Takahashi M., Chiba Y., Murakami K., Ishii S., Kawai Y., Saito K.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Watanabe S., Kimura K., Nakamura Y., Nagahari K., Masuho Y.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
Ninomiya K., Iwayanagi T.;
Ninomiya K., Jayanagi T.;
Ninomiya K., Garanagi T.;
Ninomiya K., Garanagi T.;
Ninomiya K., Garanagi T.;
Ninomiya K., Garanagi T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20264357; PubMed=10802645;
Camaschella C., Roetto A., Cali A.,
Carella M., Majorano N., Totaro A.,
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MEDLINE=21213521; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood 97:2555-2560(2001).
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Cali A., De Gobbi M., Gasparini P., Camas
New muatations inactivating transferrin
  the
                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homodimer.
SUBCELLULAR LOCATION: Type II membrane protein.
Parks the transmembrane domain and is probably:
                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: Predominantly expressed in liver. While the alpha form is also expressed in spleen, lung, muscle, prostate and peripheral blood mononuclear cells, the beta form is expressed in all tissues tested, albeit weakly.

DISEASE: Defects in TFR2 are a cause of hereditary hemochromatosis type 3 (HFE3) [MIM:604250]. HFE3 is a disorder of iron hemostasis type 3 (HFE3) in iron overload and has a phenotype indistinguishable resulting in iron overload and has a phenotype indistinguishable from that of hereditary hemochromatosis (HH). HH is characterized by abnormal incestinal iron absorption and progressive increase of total body iron, which results in middlife in clinical total body iron, which results in middlife in clinical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
                                                                                           hemochromatosis type III affects the putative initiation the beta isoform thus preventing its translation. SIMILARITY: BELONGS TO PEPTIDASE FAMILY MZ8B.
                                                                                                                                                                                          complications including cirrhosis, cardiopathy, diabetes, endocrine dysfunctions, arthropathy, and susceptibility to cancer. Since the disease complications can be effectively prevented by regular phlebotomies, early diagnosis is most important to provide a normal life expectancy to the affect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genet.
                                                                                                                                                     MISCELLANEOUS: The variant lys-172 found in hereditary
                      European
                                    SWISS-PROT entry is copyright. It is produced through a collaboration -
een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q9UP52-2; Sequence=VSP_005354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9UP52-1; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9UP52-3;
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. 8:1060-1073(1998).
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                      Swiss Institute of Bioinf
Bioinformatics Institute.
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., Camaschella C.;
sferrin 2 in hemochromatosis
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EMBL; AF053356; AAC78796.1;
EMBL; AK022002; BAB13951.1;
EMBL; AK000421; BAA91153.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005887; C:integral to plasma membrane; NAS GO; GO:0004998; F:transferrin receptor activity; Ni GO; GO:0006826; P:iron ion transport; NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGSAPPDSSWRGSLKVS-YNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRYVILGGHRDSWVEGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPVAPQE--WQGSLLGSPYHLGPG-----PRLRLVVNNHRTSTPINNIFGCIEGRSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHYVVIGAQRDAWGPGAAKSAVGTAILLELVRTFSSMVSNGFRPRRSLLFISWDGGDFGS
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                                                                                                                                                                                                                                                                                                         YPLYHSVYETYELVEKFYDPMF-KYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKY
                                                                                                                                                                                                                                                                                                                                                                             SGQTLYEQVVFTNPSWDAEVIRPLPMDSSAYSFTAF---VGVPAVEFSFMEDDQ-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                       EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGSTEWLEGYLSVLHLKAVVYVSLDNAVLGDDKFHAKTSPLLTSLIESVLKQVDSPNH---
                                                          LMFLERAFIDPLGLP-DRPFYRHVIYAPSSHNKYA-
                                                                                                                                                                                 ADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMNDQ
                                                                                                                                                                                                                                               YPFLHTKEDTYENLHKVLOGRLPAVAQAVAQLAGQLLIRLSHDRLLPLDFGRYGDVVLRH
IMRVEFYFLSQYVSPADSPF-RHIFMGRGDHTLGALLDHLRLLRSNSSGTPGATSSTGFQ 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         801 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.98;
                                                                                                                              -GDLKARGLTLQWVYSARGDYIRAAEKLRQEIYSSEERDERLTRMYNVR
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
Missing (in isoform B
Missing (in isoform B
MISSING (in isoform B
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Pred. No. 1.]
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R -> RIPLSAQV (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform /FTId=VSP_005355.
M -> K (IN HFE3).
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INTERCHAIN (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> KIPLSAQV (IN REF. 2)
D3D3082BA835413A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta).
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                                                                             -GESFPGIYDALFDI
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----FRRQLALLTWTLQGAANALS

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ALD PART REPORTED TO THE PROPERTY OF THE PROPE
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Battlov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrind L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RI Nature 409:685-690(2001).
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TFR2_MOUSE
                              Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Malaby S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20160931; PubMed=10681454; MEDLINE=20160931; PubMed=10681454; Fleming R.E., Migas M.C., Holden C.C., Waheed A., Britton R.S., Tomatsu S., Bacon B.R., Sly W.S.; "Transferrin receptor 2: Continued expression in mouse liver in face of iron overload and in hereditary hemochromatosis."; Proc. Natl. Acad. Sci. U.S.A. 97:2214-2219(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Liver; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawabata H., Germain R.S., Ikezoe T., Tong X., Green E.M., Gombart A.F., Koeffler H.P.; "Regulation of expression of murine transferrin receptor 2."; Blood 98:1949-1954(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Erythroleukemia;
MEDLINE=21426540; PubMe
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               McKernan
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           Malek J.A.,
Casavant T.L., Cunner C., Carninci P., Prange C., Abramson R.D., Mullahy S.J., Abramaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muridae; Murinae;
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Pram,
Transmembrane; ...
Alternative splicing.
1 81

pfam; pF04389; Peptidase_M28;
pfam; pF04253; TFR_dimer; 1.
Transmembrane; Glycoprotein;

Receptor; Signal-anchor; CYTOPLASMIC (POTENTIAL)
SIGNAL-ANCHOR (TYPE-II |

(TYPE-II MEMBRANE PROTEIN)

. .

Pfam;

InterPro; IPR003137; PA. Pfam; PF02225; PA; 1.

MGD; MGI:1354956; Trfr2.

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EMBL; AF222895; AAF37272.1; --
EMBL; AF207741; AAL05976.1; --
EMBL; AF207742; AAL05977.1; --
EMBL; AK004965; BAB23705.1; --
EMBL; AK004848; BAB23614.1; --
EMBL; BC013654; AAH13654.1; --
EMBL; AF312033; AAK28830.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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"Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 1922 with the orthologous region on mouse chromosome 5.", nucleic Acids Res. 29:1352-1365(2001).

1- FUNCTION: Mediates cellular uptake of transferrin-bound iron in non-iron dependent manner. May be involved in iron metabolism, hepatocyte function and erythrocyte differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk Svillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Sunterfield Y.S.N., Krzywinski S., Myers M.A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed in kidney, spleen, brain, lung, heart and mu very low expression in kidney, muscle and heart. DEVELOPMENTAL STAGE: First expressed beween embryo day In the liver, expression increases during development day 13 to adulthood while, in the spleen, levels remained to the spleen of the sple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=3;
IsoId=Q9JKX3-3; Sequence=VSP_005356;
TISSUE SPECIFICITY: Predominantly expressed in liver. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            throughout development.
INDUCTION: Down-regulated during erythrocyte differentiation.
Expression unchanged by cellular iron status.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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Note=Lacks most of the extracellular
confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9JKX3-2;
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                                                                                                                                                                                                                                                                                                                                                                                                                              s requires a license agreement (See an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.isb-sib.ch/announce/
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NCBI_TaxID=10116; [1]
                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                          Rattus norvegicus (Rat).
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                                                                                                                                                                             GAASSRLTAGLGFQESRFRRQLALLTWTLQGAANALS 788
                                                                                                                                                                                                                                                                                                                                     YPLYHSVYETYELVEKFYDPMFKYHL----TVAQVRGGMVFELANSIVLPFDCRDYAVV
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                                                              (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Last annotation update)
(receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (Fragment).
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ENDOCYTOSIS SIGNAL (POTENTIAL).
INTERCHAIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
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                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TISSUE-Testis;
MEDLINE-91125359; PubMed-2126342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roberts K.P., Griswold M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous system (By similarity).
SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin molecule per polypeptide chain (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
TISSUE SPECIFICITY: In testis, expressed in Sertoli cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        release. The apotransferrin-receptor complex is then recycled to the cell surface with a return to neutral pH and the concomitant loss of affinity of apotransferrin for its receptor. Transferrin receptor is necessary for development of erythrocytes and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peritubular myoid cells and Sertoli cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A34549; A34549.
  234
                                                                                                                                                                                                                                                                                                                                                                                    211 MEGNCPPSWNIDSSCK--LELSQN---
                                                                                                                                                                                                                                                                        258 YEEPDRYIVVGAQRDAWGPGVAKSSVGTGLLLKLAQVFSDMISKDGFRPSRSIIFASWTA
                                                                                                                                                                                                                                                                                                          57 AVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFG-TLKKEGWRPRRTILFASWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                   PDEGFEGKSLY--ESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNW
                                                                                                                                                            GDYGAVGPTEWLEGYLSSLHLKAFTYINLDKVVLGTSNFKVSASPLLYTLMGKIMQDVKH
                                                                                                                                                                                         EEFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKS
                                                                                                                                                                                                                                                                                                                                                                                                                                        MGGSAPP----DSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRG
ETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYA
                                                        P---IDGKYLYRNSNWISK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1431
508
109
113
179
584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Receptor; Lipoprotein; Palmitate; Endocytosis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptidase_M28; 1.
TFR_dimer; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622
510
109
113
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584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.1%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70152 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIGAND-BINDING (BY SIMILARITY).

CELL ATTACHMENT SITE (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (BY SIMILARITY.

N-LINKED (GLCNAC...) (BY SIMILARITY.

N-LINKED (GLCNAC...) (BY SIMILARITY.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 445.5; Pred. No. 1.5e
89; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       831E4FC16DE55703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in germinal cells. Highest levels
                                                   ---IEELSLDNAAFPFLAYSGIPAVSFCFCED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180;
                                                                                                                                                                                                                                                                                                                                                                                    -QNVKLTVNNVLKETRILNIFGVIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                               377
                                                                                                                                                                                                                        175
  293
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RESULT 14
TFR1_CANF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parker J.S.L., Murphy W.J., Wang D., O'Brien S.J., Parrish C.R.;

"Canine and feline parvoviruses can use human or feline transferrin

"receptors to bind, enter, and infect cells.";

"L. J. Virol. 75:3896-3902(2001).

"C. -!- FUNCTION: Cellular uptake of iron occurs via receptor mediated endocytosis of ligand-occupied transferrin receptor into specialized endosomes. Endosomal acidification leads to iron release. The apotransferrin-receptor complex is then recycled to the cell surface with a return to neutral pH and the concomitant conceptor is necessary for development of erythrocytes and the nervous system (By similarity).

"C. --- SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin conceptor is necessary for development of entransferrin metals."
 Pfam; PF04389; Peptidase_M28; 1.

Pfam; PF04389; Peptidase_M28; 1.

Pfam; PF04253; TFR dimer; 1.

Transmembrane; Glycoprotein; Receptor; Lipoprotein; Palmitate;
Signal-anchor; Endocytosis; Phosphorylation.

Signal-anchor; Endocytosis; Phosphorylation.

CYTOPLASMIC (POTENTIAL).

TRANSMEM 71 90 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                     entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21165299; PubMed=11264378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFR1_CANFA
                                                                                                                                                                                                tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                    similarity).
MISCELLANEOUS: Canine and feline
                                                                                                                                                                                                                                                                                                                                                                                                                  molecule per polypeptide chain (By similarity). SUBCELLULAR LOCATION: Type II membrane protein PTM: N. and O-glycosylated, phosphorylated and
                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                       feline transferrin receptors and infect cells.
                                                                                                                                              AF297626; AA(
P02786; 1CX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478
                                                                                                            PF02225; PA; 1
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                                                                                                                                IPR003137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIESKYDPSKAWGDVKRQISVAAFTVQAAAETLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHN-----KYAGESFPGIYDALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKLLSFMKDLNQFK----ADIKDMGLSLQWLYSARGDYFRATSRLTTDFHNAEKTNRFVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EDYPYLGTKLDTYEILIQKVPQLNQMVRTAAEVAGQFIIKLTHDIELTLDYEMYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REINDRIMKVEYHFLSPYVSPRESPFRHIFWGSGSHTLSALVENLRLRQKNITAFNETLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
receptor protein 1 (TfR1) (TR)
                                                                                                                                                                  AAG24850.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                              rmatics Institute. There are no restrictions institutions as long as its content is in
                                                                                                                                PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                     use these
                                                                                                                                                                                                                                                                                                                                                                                      parvoviruses bind human and
                                                                                                                                                                                                              (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
(TR) (TfR) (Trfr).
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                                                                                                                                                                                                                                                                                                                                                                       receptors to enter
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RESULT 15
TFR1_MOUSE
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                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                        Transpersor TREE.

Mus musculus (Mouse).

Mus musculus (Metazoa; Chordata;

Metazoa; Rodentia;

Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
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LIPID
MOD_RES
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
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DOMAIN
SITE
SITE
SITE
                                                                                                                                                                                          MOUSE
                                                      Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                                                                                                                                                              TFR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                    682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQK-VKMHIHSTNEVTRIYNVIGTLRGAVE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                     NKSAFNETLLRNQLALATWTIQGAANALS
                                                                                                                                                                                                                                                                                                                                                    RKYADKIYNISMKHPQ---EMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILL
                                                                                                                                                                                                                                                                                                                                                                              --TDYPYLGTTMDLYENLNQKIPQLNKMARGAAEVAGQLIMKLTYDLELNLN-----Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDE 178
                                                                                                                                                                                                                                                                                                         RMMNDQLMFLERAFIDPLGLP-DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVD 412
                                                                                                                                                                                                                                                                                                                                                                                                                                            GFEGKSLY--ESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTL-KKEGWRPRRTILFASWDAEEF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEGDCP--SAW-----EIDPSCRLETSSNKNVNLTVNNVLKEIRIFNVFGVIKGFEE 408
                                                                                                                                                                                                                                                           PSKAWGD--VKRQISVAAFTVQAAAETLS
                                                                                                                                                                                                                                                                                  REINDRIMKVEHNFLSPYVSPRDSPF-RHIFWGSGSH-----TLPALVEHL---KLRQK
                                                                                                                                                                                                                                                                                                                                 EMYNDRILSFVRDMNQFRTDIKEMGLNLQWLYSARGDFFRATSRLTTDYKNAERTNRFVM
                                                                                                                                                                                                                                                                                                                                                                                                   KFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVL
                                                                                                                                                                                                                                                                                                                                                                                                                            -ITGQSLYRDSNWINK-----VEKLSLDNAAFPFLAYSGIPAVSFCFCED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAIGATEWLEGYLSSLHLKAFTYINLDKAILGTSNFKVSASPLLYSLLEKTMKDVKHP--
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337
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27.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O-LINKED (GÂLNAC. . .) (BÝ SIMILARITY).
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (BY SIMILARITY).
N-LINKED (GLCNAC. . . .) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 445.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STOP-TRANSFER SEQUENCE
CELL ATTACHMENT SITE (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENDOCYTOSIS SIGNAL
                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                            763
                                                                                                                                                                                                                                                           439
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                                                                                                                 (TfR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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STRAIN=C57BL/6 X DBA/2; TISSUE=Hematopoietic; Trowbridge I.S., Domingo D.L., Thomas M.L., Chain A.; Submitted (JAN-1991) to the EMBL/GenBank/DDBJ databases.

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SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE OF
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sequence.";
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J. Immunol. 134:3474-3479(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-85159078; PubMed=2984291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the nervous system.";
Nat. Genet. 21:396-399(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99206608; PubMed=10192390;
Levy J.E., Jin O., Fujiwara Y., Ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecule per polypeptide chain (By similarity).
-i- SUBCELLULAR LOCATION: Type II membrane protein
-i- PTM: N- and O-glycosylated, phosphorylated and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION
                                                                                                                                                                                                     DOMAIN
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Transferrin receptor is necessary for
                                                                                                                                                         SITE
                                                                                                                                                                           SITE
                                                                                                                         TIPID
                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                   Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                       Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IP
Pfam; PF0222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Cellular uptake of iron occurs via receptor-mediated endocytosis of ligand-occupied transferrin receptor into specialized endosomes. Endosomal acidification leads to iron release. The apotransferrin-receptor complex is then recycled to the cell surface with a return to neutral pH and the concomitant loss of affinity of apotransferrin for its receptor. Transferrin receptor is necessary for development of erythrocytes and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ), MGI:98822; Trfr.
GO:0006879; P:iron ion homeostasis; IMP
erPro; IPR003137; PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nervous system (By similarity).
SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S29548; S29548.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PF04389;
                                                                                                                                                                                                                                                                                                                                                                                                       PF04253;
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                                                                                                                                                                                                                                                                                                                                                                        Peptidase_M28; 1.
TFR_dimer; 1.
Glycoprotein; Rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PA;
                                                                                                                                                                                                                                                                                                                                                         Endocytosis;
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24
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98
                                                                                                                                                                                                                                                                                                                                 Phosphorylation.
CYTOPLASMIC (POTENTIAL)
  PHOSPHORYLATION (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
O-LINKED (GALNAC...) (BY SIMILARITY).
N-LINKED (GLCNAC...) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                Receptor; Lipoprotein; Palmitate
                                                                                                                            STOP-TRANSFER SEQUENCE.
CELL ATTACHMENT SITE (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                          ENDOCYTOSIS SIGNAL
                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
LIGAND-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                          SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                     (POTENTIAL).
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     (GALNAC. . .) (BY SIMILARITY). (GLCNAC. . .) (BY SIMILARITY).
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                                                                                                                                                                                                                                          174 KSPDEGFEGKSLY--ESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTK 231
                                                                                                                                                                                                                                                                                                                          398
                                                                                                                                                                                                                                                                                                                                                                                                                                     123;
729
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                                                                                                                                                                                                                                                                                                                                                                              MEGSCPARWNIDSSCK--LELSON------QNVKLIVKNVLKERRILNIFGVIKG
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                       IYDALFDIESKVDPSKAWGDVKRQISVAAFTVQAAAETLS
                                                                             SNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHN----
                                                                                                        YNSKLLSF-----MKDLNQFKTDIRDMGLSLQWLYSARGDYFRATSRLTTDFHNAEK
                                                                                                                                                                                    NWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRD
 FNETLE
                                                  TNRFVMREINDRIMKVEYHFLSPYVSPRESPFRHIFWGSGSHTLSALVENLKLRQKNITA
                                                                                                                                   YAVVLRKYADKIYNISMKHPQEMKT----YSLSFDSLFSAVKNFTEIASKFSERLQDFDK
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                                                                                                                                                                                                                  KHP---VDGKSLYRDSNWISK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.7%;
26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (B1 54...)
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (BY SIMILARITY).
LA -> AL (IN REF. 2).
W -> H (IN REF. 3; AA SEQUENCE).
W -> I (IN REF. 3; AA SEQUENCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
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Search completed: October 4, 2003, 23:22:06
Job time: 36 secs

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Result
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ALIGNMENTS

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PUBMED	MEDLINE	JOURNAL	TITLE	AUTHORS	REFERENCE	PUBMED	MEDLINE	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION			DEFINITION	LOCUS	AK002920
11042159	20499374	prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617–1630 (2000)	Normalization and subtraction of cap-trapper-selected cDNAs to	<pre>Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.</pre>		10349636	99279253	Meth. Enzymol. 303, 19-44 (1999)	High-efficiency full-length cDNA cloning	Carninci, P. and Hayashizaki, Y.	ı	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus	Mus musculus (house mouse)	HTC; CAP trapper.	AK002920.1 GI:12833258	AK002920	sequence.	library, clone:0610042N21 product:FOLATE HYDROLASE, full insert	Mus musculus adult male kidney cDNA, RIKEN full-length enriched	AK002920 3003 bp mRNA linear HTC 05-DEC-2002	

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COMMENT
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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3003)
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Shibata,K.,
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                                                                                                    ACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCTT
                                                                                                                                                                                                                                 TGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAGC 540
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                                                                                                                                                                                                                                                                                                                                                                         AGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAACGTGGAAATGTCTTAAATCTTAATGGTGCAGGTGACCCGCTCACACCAGGTTACCC
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62.9%;

Score 1253.4; Pred. No. 1e-1: 0; Mismatches

le-159;

Indels

0;

Gaps

776

480 896 420

956

600 1076

1016

DB 11; 241;

Length 3003;

0,

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cleaved with XhoI and SstI. Cloning sites, 5' end: SstI;
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//db_XTEf="MGI:1858193"
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//tanslation="MWNALQDRDSAEVLGHRQRWLRVGTRYDHLAGTQNNFELAKQIHDQW
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PPYSAFSPQGTPEGDLVYVNYARTEDFFKLEREWKISCSGKIVIALRGAGDPLTPGYPA
NGLAGAKGMILYSDPADYFVPAVKSYPDGWNLDGGGVQROVLALRUGAGDPLTPGYPA
NGLAGAKGMILYSDPADYFVPAVKSYPDGWNLDGGGVQROVLALRUGAGDPLTPGYPA
NGLAGAKGMILYSDPADYFVPAVKSYPDGWNLDGGGVQROVLALRUGAGDFUTPGYPA
NGHAYRHELTNAVGLPSIPVHPIGYDDAGKLEHMGGAPPDSSWKGGLKVPYNVGPG
FAGNRSTQKVWMHIHSYTKVTRIYNVIGTLKGALEPDRYVILGGTBWAEEGIDPQS
GAAVVHEIVRSFGTLKKKGRRRRTILFASWDAEEFGLLGSTEWAEEHSRLLQERGVA
YINADSSIEGNYTLRVDCTPLMYSLVTLTKELLGSPDEGFEGKSLYDSWKEKSPSPEF
IGMPRISKLGSGNDEFFYFGRALGIASGRARYTKNWKTNKVSSYPLYHSVETYFELVVK
FYDPTFKYHLTVAQVRGAMVFELANSIVLFSCOSYAVALKKYADTIVNISMKHPQEM
                                                        KAYMISFDSLFSAVNNFTDVASKFNQRLQELDKSNPILLRIMNDQLMYLERAFIDPLG
LPGRPFYRHIIYAPSSHNKYAGESFPGIYDALFDISSKVNASKAWNEVKRQISIATFT
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/strain="C57BL/6J"
/strain="C57BL/6J"
/db_xref="raNTOM_DB:0610042N21"
/db_xref="MGI:1907173"
/db_xref="taxon:10090"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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(SPTR|Q9DCC2, evidence: FASTY, 100%ID, 100%length)
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CTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTGT	241 GGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTGA 300	Query Match 60.5%; Score 1205.6; DB 11; Length 2948; Best Local Similarity 85.3%; Pred. No. 2.8e-153; Matches 1379; Conservative 0; Mismatches 234; Indels 3; Gaps 3;	904	i	h, match=2256)		/db_xref="FANTOM_DB:G630038H05" /db_xref="taxon:10090" /clone="630038H05" /tissus type="cortex"	12948 /organism="Mus musculus" /mol_type="mRNA" /strain="C57RI/6."	Please visit URL:http://g URL:http://f	Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) CDNA library was prepared and sequenced in Mouse Genome	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho. Tsurumi-ku, Yokohama.	Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,	Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Koilma,Y., Kondo,S., Konno,H., Kouda,M.,	of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2948) Adachi.J. Alzawa.K. Akimura.T. Arakawa.T. Bono.H. Carninci.P.	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation	Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851	Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5903.r
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODN001AF07QP1&cluster=5903.r. Cont
Feng Liang Email : flang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 160
Faraday Avenue Genoscope sequence ID : CSODN001AF07QP1.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pcMVSPORT_6; lst strawas primed with a NotI-oligo(dT) primer. Five primer enriched, double-strand cDNA was digested with Not enriched with Not I and Ecory sites of the pcMV?
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CS0DM001YE22
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced
Contact: Genoscope
Genoscope Centre National de Sequencage
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AL563970.2 GI:31287955
EST.
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Email: seqref@enoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5903.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgi-bin/cluster.cgi?seq=CSODM001BC11NP1&cluster=5903.r. Contact Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen.Com/ Corporation 1600
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Location/Qualifiers
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/note="Organ: liver; Vector: pcMVSpORT_6; lst strand cDNA
/note="Organ: liver; Vector: pcMVSpORT_6; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV stres of the pcMVSPORT 6
vector. Library was not normalized."
251 c 212 g 333 t 63 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="fetal"
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92.2%;
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AL532691.2 GI:3107052
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Euteleostomi;

EST 23-MAY-2003

1920

90

Qy 931 AGAGCGTGGCGTTATATTATGCTGACTCTATAGAAGAAACTACACTCTGAG 1	about this cluster, see cope.cns.fr/ cope.com URL: fliang@lifetech.com URL: cope.com URL: cope.com InVitroGen Corporation 1600 noscope sequence ID: CSODNOO1AF07NP1. cope.com InVitroGen Corporation 1600 cope.com InvitroGen Corporation 1600 cope.com InvitroGen Corporation 1600 cope.com InvitroGen Corporation 1600 cope.com InvitroGen InvitroGen Corporation 1600 cope.com InvitroGen I	JOURNAL Unpublished COMMENT On Feb 13, 2001 this sequence version replaced gi:12796184. Contact: Genoscope Genoscope - Centre National de Sequencage Bp 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5903.r For
RESULT 6 CA489536 CA489536 CA489536 CA489536 DEFINITION AGENCOURT_10810626 MAPCL Homo sapiens cDNA clone IMAGE:6722010 5', DEFINITION MRNA sequence. CA489536.1 GI:24952327 CA89536.1 GI:24952327 REYMORDS FORGANISM CA489536.1 GI:24952327 CA89536.2 Homo sapiens (human) ORGANISM ENKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS NIH-MGC http://mage.nci.nih.gov/ Tissue Procurement: Krausberg, Ph.D. Email: Capabs-remail.nih.gov Tissue Procurement: Kristi A. Egland, Ira Pastan COMMENT CONA Library Arrayed by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM14284 row: a column: 18	Db 461 Qy 1470 Db 401 Qy 1530 Db 341 Qy 1590 Db 298 Qy 1650 Db 298 Qy 1710 Db 254 Qy 1770 Db 114 8 Qy 1889 Db 74 Db 1947	Db 581 AAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCAAGGTTCGAGGAGGGA 522 OY 1350 TGGTGTTTGAGCCTAGCCAATTCCATAGTGCTCCCTTTTGATTGTCGAGATTATGCTGTAG 1409

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                                                      ACAGTTTATCATTTGATTCACTTTTTTCTGCAGTAAAAAATTTTTACAGAAATTGCTTCCA 1535
                                                                                                    GAAAGTATGCTGACAAAATCTACAATATTTCTATGAAACATCCACAGGAAATGAAGACAT 1475
AGTTCAGCGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATATTGTTAAGAATGATGA 1595
                                            ACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTTTACAGAAATTGCTTCCA
                                                                                         GAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAAATGAAGACAT
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Manuscript submitted."
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/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
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/mol_type="mRNA"
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Pred. No. 1.6e-102;
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                                                                                          Similarity
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CA976138
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Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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AAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCTTGGTATACAACCTAAC
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                                                                         Conservative
                                                                                                                                                                          /tissue_type="sciatic nerve"
//dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sciatic_nerve"
/note="Yector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGACCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Mammalia; E
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Leventhal, C., McElligott, K., Boozer, S., Mays, R., Smith, Lerner, L., Costa
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Creation of genome-wide protein expression activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)
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                TGGACCCTTCCAAGGCCTGGGGAGATGTGAAGAGACAGATTTCTGTTGCAGCCTTCACAG
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/note="See 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
a 157 c 127 g 262 t
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Tel:
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Creation of genome-wide protein expression libraries using random activation of gene expression
Mat. Biotechnol. 19 (5), 440-445 (2001)
                                ACTCTACCAATGAAGTGACGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGG
                                                                                        ACAATGTTGGACCTGGCTTTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCC
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; I
1 (bases 1 to 767)
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D.,
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Scott J.
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21227151
             ACTCTACCAATGAAGTGACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGGAGTGG
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RST13413 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG194269 BG194269.1 GI:13715956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scain@athersys.com
                                                                                                                                                                                                                                                                     Libraries using Random Activation of Gene Expression', Nature Blotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
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98.3%;
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DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 864 Std Error: 0.00
                                                                                                                                                Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                        Tissue Procurement: David
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                       AI050871 770 bp mRNA linear EST 24-SEP-1998 0947bll.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1668957 3', similar to qb:M99487 PROSTATE-SPECIFIC MEMBRANE ANTIGEN (HUMAN ):contains Alu repetitive element;, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                         cDNA Library Preparation: M. Bento Soares,
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d N. Louis, M.D.,
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Sequencing Center information can be

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                AGAGACTCTGTATTGAATTTGTGTGTGTATGTCACTC - - AAAGAATAATAATGGGTATATT
                                                        AGCCTTCACAGTGCAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGGGATTCTTT 1866
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  primer: -40ml3 fwd. ET from Amersham
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/clone="IMAGE:1668957"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
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Creation of genome-wide protein expression libraries using random activation of gene expression

activation of gene expression
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RST22191 Athersys RAGE Library Homo
BG202823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: scain@athersys.com
High quality sequence stop: !
Location/Qualifiers
1. .797
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Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Scott J. Cain
Athersys, Inc.
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GGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGC 1206
                                                                                                         AGTTGGACTAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGG-ATAAGCAAAATT 1146
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/Colone_lib="Athersys RAGE Library"
/Colone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
/note="See 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

151 c 159 g 230 t 1 others
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/db_xref="taxon:9606"
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                         Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       607
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                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: David N. Loui
                   info@image.llnl.gov
Seq primer: -40UP from Gibco
                                                                                                                                                                          1 (bases 1 to 720)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                        BF940223 720 bp mRNA linear EST 22-JAN-2001 nac70c04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:4439495 37 similar to SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                                                                      cDNA Library Preparation: M. Bento
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                                                                                                                          N. Louis, M.D., Myrna R.
                                                                                                    Soares,
                                                                                                   Ph.D.,
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                                                                                                                                                  CTGTTTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGAAGTGAAGAGACAG
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96.9%;
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181

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361

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/tissue_type="glioblastoma/lab_host="DH10B"
                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3439495"
                                                                                                                                                                /organism="Homo sapiens
Score 674.6; Pred. No. 1.4e
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similar to gb:M99487 PROSTATE-SP
mRNA securer
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Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 690)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anal
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 454.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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AI672408
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2283910"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone_lib="NCI_CGAP_Kidl1"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132336-1323911, 1456007-1456775, and forescaled the same of the same in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fatima Bonaldo.
152 c 110
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95.7%;
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1644 TACCAGACAGACCTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACCAACAAGTATG
                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Kristi A. Egland, Ira Pastan

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate.rlmAd270
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6720185"
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UI-H-COO-ark-a-12-0-UI.Sl NCI_CGAP_Sub9 Homo sapiens
UI-H-COO-ark-a-12-0-UI 3', mRNA sequence.
                                                              Eukaryota;
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mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 606)
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a 169 c 211 g 249 t 1 others
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Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@illowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-73, >AT_rich#Low_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                AGCAACCCAATATTGTTAAGAATGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTT 1627
                                                                                                                                                                                                                                                                                           GTAAAAAATTTTACAGAAATTGCTTCCAAGTTCAGCGAGAGACTCCAGGACTTTGACAAA 1567
                                                                                                                                                                                                                                                                                                                                                                                     ATGAAACATCCACAGGAAATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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National Cancer Institute, Cancer Genome Anat
                                                                                                                           AGCAACCCAATAGTATTAAGAATGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTT
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Pred. No. 3.7e-67;
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ALIGNMENTS

AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	RESULT 1 AF261715
O'Keefe, D.S., Bacich, D.J. and Heston, W.D.W. Cloning and Characterization of a novel glutamate-preferring	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to.1992)	Homo sapiens (human) Homo sapiens		AF261715.1 GI:11078563	AF261715	(PSMAL/GCP III) mRNA, complete cds.	Homo sapiens prostate-specific membrane antigen-like protein	AF261715 1992 bp mRNA linear PRI 02-NOV-2000	

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O'Keefe, D.S., Ba
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(bases 1 to 1992)
('Keefe, D.S., Bacich, D.J. and Heston, W.D.W.
CYKeefe, D.S., Bacich, D.J. and Heston, W.D.W.
Expression Profile of Prostate-Specific Membrane Antigen-Like Tissues, Prostate Cancer and Tumor Associated-Vas
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/function="N-acetylated-alpha-linked-acidic dipeptidase"
/function="glutamate carboxypeptidase III; similar to Homo
/note="glutamate carboxypeptidase III; similar to Homo
sapiens PSMA; folate hydrolase-like; member of the M28
peptidase family; formed by duplication of the PSMA gene
/codon_start=1
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/protein_id="AAG29102.1"
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/tissue_type="
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Query Match 85.5%; Score 1702.6; DB 6; Length 2653; Best Local Similarity 98.5%; Pred. No. 0; Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1; Qy 240 AGGTTAAAAATGCCCAGCTGGCAGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG 299 [FEATURES Location/Qualifiers 1. 2653 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" BASE COUNT 782 a 524 c 640 g 707 t ORIGIN		Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hon E 1 C VINC B F ANGUSTIC M CONTON OF PROPERTY OF PROPER	AX337498 AX337498 2653 bp DNA linear PAT 09-JAN-2002 DEFINITION Sequence 8007 from Patent WO0194629. ACCESSION AX337498 VERSION AX337498.1 GI:18128217		Qy 1921 TATTGATAAATTTTAAAATTGGTATATTGAAATAAAGTTGAATATTAT	1861 TTCTTTAGAGACTCTGTATTGAGATTTGTGTGGTATGTCACTCAAAGAATAATAATGGGTA 19	1801 1801	QY 1741 TGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGATGTGAAGAGACAGATTTC 1800	Qy 1681 TCCAAGCAGCACAACAAGTATGCAGGGGGAGTCATTCCCAGGAATTTATGATGCTCTGTT 1740	Qy 1621 AGCATTTATTGATCCATTAGGGTTACCAGACAGACCTTTTTATAGGCATGTCATCTATGC 1680	Qy 1561 TGACAAAAGCAACCCAATATTGTTAAGAATGATGAATGATCAACTCATGTTTCTGGAAAG 1620	Qy 1501 TTCTGCAGTAAAAAATTTTACAGAAATTGCTTCCAAGTTCAGCGAGAGACTCCAGGACTT 1560	Qy 1441 TATTTCTATGAAACATCCACAGGAAATGAAGACATACAGTTTATCATTTGATTCACTTTT 1500
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1210 ACMIDICIANGAMACATAIGNOTIGOGOGAAAAGTTTTAIGATCCAAIGTTTAAATAIC 1319		1080 TTTATGAAAGTTGGACTAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAA 1139	1619 ACTCATCTATAGAAGGAACTTAAAACTACACCCTGATGATGATCTACCCGCTGATGAAGCT 1678 1020 TGGTATACAACGTAAAAAGAGCCTGAAGAGCCCTGATGAAGGCATTTGAAGGCAAATCTC 1079 1021 TGGTATACAACGTAAAAAGAGCCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC 1079 1031 TGGTACACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC 1738	900 AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTG 959	840			1259 TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACCCAC	1199 CACCACCAGATAGCAGCTGGAGAGGAGGTCTCAAAGTGCCCTACAATGTTGGACCTGGCT 1258 600 TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACACTCCACTCTACCAATGAAGTGA 659	1139 CTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG 1198 540 CACCACCAGATAGCAGCTGGAGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT 599	1079 CAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTCGTTGGTCTTCCAAGTATTC 1138 480 CTGTTCATCCAGTTGGATACTATGGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG 539	1019 TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTACC 1070 420 CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC 479	959 ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGATGGTTGGAATCTTCCTGGAGGTGGTG 1018 360 TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGCTTACC 419	899 AGGTTAAAAATGCCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCCGACCCTGCTG 958

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Sequence 1 from Patent W00240059.
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AX505108.1 GI:23386415
                                                               American Foundation for Biological Research
Milcho S. (US); Loukinov, Dmitri I. (US);
Location/Qualifiers
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Patent: WO 0240059-A 1
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PREFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQ AAAETLSEVA" 1 524 c

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JOURNAL Patent: US 5538866-A 1 23-JUL-1996;
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhii 1 (bases 1 to 2653)
Israeli, R. S., Powell, C. T., Fair, W. R. ar Molecular cloning of a complementary DN prostate-specific membrane antigen Cancer Res. 53 (2), 227-230 (1993) 9313576
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CAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC
                  CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC
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FSLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPP
FSAFSPGGMBEGDLVYUNYARFEDFFKLERDMKINCSCKIVIARYGKVFHONKYKKAQ
LAGAKGVILYSDPADYFAPGVKSYPDGWNLPGGGVQRGNILNLNGAGDPLTPGYPANE
YAYRRGIAEAVGLPSIPVHPIGYYDAQKILEKMGGSAPPDSSWRGSLKVPVNVGFGTD
GNETTGKVKMHIHSTNEVTRIYNIGTIRGAVEPBRYVILGGHRDSWYFGGTDPQSGA
AVVHEIVRSFGTLKKEGWRPRRIILFASWDAEEFGLLGSTEWAEENSLLQERGVAYI
NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEKSLKESWTEKSPEPESG
MPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFY
DPMFKYHLTVAQVRGGWYFELANSIVLPFDCRDYAVVLKKYADKIYSISWKHPQEWKT
YSVSFDSLFSAVKNFTEIASKFSERLQDFDKSNPIVLRMNDQLMFLERAFIDPLGLP
DRAFKYHTVAPASSHNKYAGESFPGIYDALFDISKVDPSKAWGEVKROITVAAFTVQ
DRAFKYHTYAPSSHNKYAGESFPGIYDALFDISKVDPSKAWGEVKROITVAAFTVQ
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/product-"prostate- specific
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/codon_start=1
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/tissue_lib="LNCaP
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/cell_type="prostate"
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Direct Submission
Submitted (09-AUG-1999) Intern
California, Davis, TB 156, Dav
Location/Qualifiers
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Devlin,A.M., Ling,E.H., Peerson,J.M., Fernando,S., Csmith,A.D. and Halsted,C.H.
Glutamate carboxypeptidase II: a polymorphism associlevels of serum folate and hyperhomocysteinemia Hum. Mol. Genet. 9 (19), 2837-2844 (2000)
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/mol.type="mRNA"
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/tissue_type="small intes
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/gene="FGCP"
/codon_start=1
/codon_start=1
/product="folylpoly-gamma-glutamate carboxypeptidase"
/protein_id="AAD51121.1"
/db_xref="GI:5762482"
/translation="MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIK
                                                                                                          /gene="FGCP"
139. .2391
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Ling, E.-H.
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FSAFSPGMPEGDLVYVNYARTEDFFKLERDMKINGSGKIVIARYGKVFFGNKVKNAQ
LAGAKGVILYSDPADYEAPGVKSYPDGWILPGGGYQRGNILNLNGAGDPLTPGYPANE
YAYRRGIAEAVGLPSIPVHPIGYYDAGKLLEKMGGSAPDDSSWRGSLKVPYNVGPGFT
GNFSTQKVKMHIHSTNEVTRIYNVIGTLKGAVEPDRYVLIGGHRDSWVFGGIDPGSGA
AVVHEIVRSFGTLKKEGWRPRFRILFASWDAEEFGLLGSTEWAEENSRLLQEFGYAXI
NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKKSPSPEFSG
MPRISKIGSGNDFEVFFQRLGIASGRARYTKNWETNKFSCYPLYHSYVETYELVEKFY
DPMFKYLTVAQVRGGMYFELANSIVLFDCRDYAVVLKKYADKIYSISMKHPQEMKT
YSVSFDSLFSAVKNFTELASKFSERLQDFDKSNPTVLRMNDQLMFLERAFIDPLGLP
PREFYRHVIXAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQ
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Zhang, Z.
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                                                                                                  TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG
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Pred. No. 0;
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SSNEARINITPKHNMKAFLDELKAENIKKFLYRNTOIPHLAGTEONFOLAKOIQSGWKE
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FGLDSVELAHYDVLLSYPNKTHPNYISIINEDGENEIFWTSLFEPPPPGYKENVSDIVVPP
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GNESTOKVKMHIHSTNEVTRITWNIGTLEGAVEPDRYVILGGHRDSWVFGGIDPQSGA
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NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFBGKSLXVESWTKKGPSPEFSG
MPRISKLGSGNDFEVFFORLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFY
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YSVSFDSLFSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYHHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQ
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/protein_id="CAD42451.1"
/db_xref="GI:21900510"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Minyixue Zazhi 17 (5), 328-330 (2001) 2 (bases 1 to 2253) Ye,C.Z. Losses 1 to 2253) Ye,C.Z. Ye,C.	1740 TTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGATGTGAAGAGACAGATTT 1799	600 998 660	Euteleostomi; Homo. membrane	ORGANISM ORGANISM REFERENCE AUTHORS TITLE
Homo saptems (Manual) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 2253) Ye,C.Z., Zhang,F.L., Zhang,Y.K. and Chen,C.Q. Cloning and sequencing of Chinese prostate-specific membrane antigen Mianyixue Zazhi 17 (5), 328-330 (2001) 2 (bases I to 2253) Ye,C.Z. Direct Submission Submitted (06 MAY-2002). Department of Urology, Zhongshan Hospital, Medical Center of Fudan University, Fenglin Rd 180, Shanghai Location/Qualifiers 1. 2253 Oy 840 Oy 840	1740 TTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGATGTGAAGAGACAGATTT 1799 111111111111111111111111111111	CAC	. 2253 bp mRNA linear PRI 27-MAY-2002 prostate-specific membrane antigen mRNA, complete cds. 1:21217742	RESULT 9 AY101595 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE
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                                                      Contact: nisc_mgc@nhgri.nih.góv
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramur Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                         Institute,
USA
Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 49 Row: e Column: 5
                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R.
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BC025672.1
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   Conservative
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/protein_id="AAH25672.1"
/protein_id="AAH25672.1"
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/db_xref="G1:1943604"
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FGLDSVELAHYDVLLSYPNKTHPNY1SIINEDGMEIFNTSLFEPPPPGYENVSDIVPP
FSAFSPQGMPEGDLYVYNVARTEDFFKLERDMKINCSGKIVIAKGAGDPLTFGVENAQ
LAGAKCVILYSDPADYEAPGVKSYPDGGWLPGGGVQRGALIALMAGAGDPLTFGVENAQ
LAGAKCVILYSDPADYEAPGVKSYPDGGWLPGGGOVQRGALIALMAGAGDPLTFGVENAQ
LAGAKCVILYSDPADYEAPGVKSYPDGGWLPGGGSAPPDSSWRGSLKVPYNVGPGFT
GNFSTQKVKMHHIHSTNEVTRIVNIGTLAGAVEDEDRYVLIGGHBOSWVFGGIDPOSGA
AVVHELVRSGGTLKKEGWFPRFTILFASWDAEEFGLLGSTEWAEENSKLLQERGVAYI
NADSGIEGNYTLKVCGWFPRFTILFASWDAEEFGKSLYESWTKKSPSPEFSG
MPRISKLGSGNDFEVFFQRLGIASGFARYTKNWETNKESGYPLYBSVYETYELPEKFY
DPMFKKHLTVAGVRGGMVFELANSIULPEDCROYAVULRKYADKIYSISMKHPQBMKT
YSVSFDSLFSAVKNFTELASKFSERLQDFDKSKHVIYAGESFPGIYDALF
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46 a 483 c 594 g 649 t
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/clone_lib="NIH_MGC_122"
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/db_xref="taxon:9606"
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                           75.98;
93.48;
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Pred. No. 0;
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                       TTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGATGTGAAGAGACAGATTT
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Patent: WO 0226984-A 2 04-APR-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                                                                                       CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG
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Eutheria;
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Primates;
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Pred. No. 6.1e-313;
D; Mismatches 6;
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  TTTCTGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCC
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Halsted, C.H., Ling, E.H.,
Gardner, J.M. and Coyle, J.
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Direct Submission
Submitted (24-FEB
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                                                             ATTACTTTGCTCCTGGGGTGCAGTCCTATCCGGATGGTTGGAATCTTCCTGGAGGGGGTG
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glarisklgscnbfeypfyricitasvvrpfdchyslyvlfryssyplthyvyrfyslysky
rybpffkyhlavaqvrggivfelansvvrpfdcholknipillekyndklynismihpqemk
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/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="jejunal mucosa"
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                                                                                                                                                                                                                                                                                                               Score 1371.6; DB 4;
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D; Mismatches 234;
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                                             TCCCTTTTGATTGTCGAGATTATGCTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACA
                                                                                       ACCTCACTGTGGCCCAGGTTCGAGGAGGGATGGTTTTGAGCTAGCCAATTCCATAGTGC
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Bzdega,T., Turi,T., Wroblewska,B.,
Direct Submission 1996) Biology, C
Submitted (23-OCT-1996) Biology, C
St. NW, Washington, DC 20057, USA
Location/Qualifiers
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a rat hippocampal cDNA library
eurochem. 69 (6), 2270-2277 (1997)
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Sciurognathi; Muridae; Murinae;
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LPGRPFYRHIIYAPSSHNKYAGESFFGIYDALFDINNKVDTSKAWREVKRQISIAAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Luthi-Carter, R., Berger, U.V., Barczak, A.K., Enna, M. and Isolation and expression of a rat brain cDNA encoding carboxypeptidase II
Proc. Natl. Acad. Sci. U.S.A. 95 (6), 3215-3220 (1998)
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Luthi-Carter,R., Berger,U.V., Barczak,A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AQLAGAKGIILYSDPADYFVPGVKSYPDGWNLPGGGVORGNULMLNGAGDDLTPGYPA
AQLAGAKGIILYSDPADYFVPGVKSYPDGWNLPGGGVORNULMLNGAGDLTPGYP
NVGPG
PAGNESHEFTEAVGLPSIPVHFIGYDDAQKLLEHMGGSAPPDSSMKGGLKVPYNVGPG
PAGNESKOKVKLHIHSYNKUTRINVIGTLGAVEDGDFVVILGGHRDAWFGGILOPQS
GAAVUHEIVFGGTLKKKKGMPRFRTILPASMDAEEFGLLGSTEWAEEHSRALDGBROR
GAAVUHEIVFGGTLKKKKGMPRFRTILPASMDAEEFGLKYDSMKEKSPSTEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="N-acetylated alpha-linked acidic dipeptidase
(NAALADase); NAAG peptidase; similar to Homo sapiene
prostate-specific membrane antigen (PSMA)"
/codon_start=1
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FYDPTFKYHLTVAQVRGAMVFELANSIVLPFDCQSYAVALKKHAETIYNISMNHPQEM
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/protein_id="AAC40067.1"
/db_xref="GI:2982229"
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Rattus norvegicus N-acetylated a
(Naalad) mRNA, complete cds.
AF513486.1 GI:21314595
                                                                                                                                                                                                                                                                   Medicine, 780-714,
                                                                                                                                                                                                                                                                           Submitted (18-MAY-2002) Department of Biochemistry, School of Medicine, Dongguk University, 707 Suk-Jang Dong, Kyungju, Kyung-Buk
                                                                                                                                                                                                                                                                                                   Park, S.Y. and Lee
Direct Submission
                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway
Rattus norvegicus
Eukaryota; Metazoa; Chorda
                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
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515 9 No. 9.8 DB 10; Length

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Search c	DЪ	Qy	DЬ	Qy	Db	Qy	Db	Qy	DЬ	Qy	Db	Qy	Db	Qy	рь	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy
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	SAGAAGTAGACTAA 2259	TGAAGTAGCCTAA 1855	AAGTGAAGAGACAGATTT 2203	ATGTGAAGAGACAGATTT 1799	GATTTATGATGCCCTTT 2143	SAATTTATGATGCTCTGT 1739	ACAGGCATATCATCTATG 2083	ATAGGCATGTCATCTATG 1679	GCTAATGTATCTGGAAC 2023	ACTCATGTTTCTGGAAA 1619	ATCAGAGACTGCAAGACT 1963	CGAGAGACTCCAGGACT 1559	ATCATTTGATTCGCTGT 1903	ATCATTTGATTCACTTT 1499	ATGCTGAGACTATCTACA 1843	ATGCTGACAAAATCTACA 1439	GGCCAATTCTATAGTGC 1783	PAGCCAATTCCATAGTGC 1379	ATCCGACATTTAAATATC 1723	ATCCAATGTTTAAATATC 1319	CAGCTATCCTCTATC 1663	CGGCTATCCACTGTATC 1259	FACTTGGAATTGCTTCAG 1603	SACTTGGAATTGCTTCAG 1199

Search completed: October 4, 2003, 19:30:45 Job time: 9499 secs

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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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        Query
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-705-477E-96
US-08-305-477E-97
US-08-394-152A-45
US-09-352-616A-454
US-09-352-553-27
US-08-324-152A-28
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US-08-325-553-9
US-08-324-468-6
US-08-822-468-6
US-08-822-468-6
US-08-823-468-6
US-08-99-965C-9
5498694-3
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GENERAL INFORMA
Sequence 97, Appl
Sequence 454, Appl
Sequence 454, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 1352, Appl
Sequence 1352, Appl
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US-08-325-553-1
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ALIGNMENTS

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application Patent No. 5538866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                         MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 17
                     ORGANISM: Homo sapiens TISSUE TYPE: Carcinoma
                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                           AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATATTAATGCTG
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                          ACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCT
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GCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAG
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                                                                    Sequence 1, Application Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: FAII, William R.
TITLE OF INVENTION: PROSTATE-SI
TITLE OF INVENTION: USES THEREO
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LI
STREET: 1185 Avenue of the AV
CITY: New York
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660 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	Qy 600 TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA 659	Qy 540 CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT 599	Qy 480 CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG 539	Qy 420 CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC 479		300 ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTG	AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG 29	Query Match 85.5%; Score 1702.6; DB 2; Length 2653; Best Local Similarity 98.5%; Pred. No. 0; Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;	FEATURE: CDS NAME/KEY: CDS LOCATION: 2622511 S-08-394-152A-1		G 1. B	LENGTH: 2653 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear	ij	NAME: White, John P. RECISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 41426-B TELECOMMUNICATION TAYOURATION		2	STATE: New COUNTRY: U ZIP: 10036 COMPUTER READ MEDIUM TYPE
QY 1740 TTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGATGTGAAGAGAGATTT 1799	QY. 1680 CTCCAAGCAGCCACAACAAGTATGCAGGGAGTCATTCCCAGGAATTTATGATGCTCTGT 1739	GAGCATTATTGATCCANTAGGCTTACCAGACAGACCTTTTTATAGGCATGTCATCTATG [1560 TIGACAAAGCAACCCAATATTGTTAAGAATGATCAATGATCAACTCATGTTTCTGGAAA 161 	1500 TTTCTGCAGTAAAAATTTTACAGAAATTGCTTCCAAGTTCAGCGAGAGACTCCAGGACT	1440 ATATTTCTATGAAACATCCACAGGAAATGAAGACATACAGTTTATCATTTGATTCACTTT 149	Qy 1380 TCCCTTTTGATTGTCGAGATTATGCTGTAGTTTTTAAGAAAGTATGCTGACAAAATCTACA 1439	Qy 1320 ACCTCACTGTGGCCCAGGTTCGAGGATGGTTTTGAGCTAGCCAATTCCATAGTGC 1379	Qy 1260 ACAGTGTCTATGAAACATATGAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATC 1319	Qy 1200 GCAGAGCACGGTATACTAAAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC 1259	Qy 1140 GCAAATTGGGAACTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAG 1199	Qy 1080 TTTATGAAAGTTGGACTAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAA 1139	Qy 1020 TGGTATACAACCTAACAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC 1079	Qy 960 ACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCT 1019	Qy 900 AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTG 959	Qy 840 GAAGAACAATTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTG 899	OY 780 CTGTTGTTCATGAAACTGTGAAGAGCTTTGGAACACTGAAAAAGGAAGG	Qy 720 TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG 779

QY 660 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	QY 600 TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA 659	QY 540 CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT 599	QY 480 CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG 539	Qy 420 CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCTTCCAAGTATTC 479	QY 360 TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACGAGGTTACC 419	35	MALCINES 1/29; CONSELVACIVE O; MISHACCIRES 24, INCELS 2, OFF 240 AGGITAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG 29 [Query Match 85.5%; Score 1702.6; DB 4; Length 2653; Query Match 98.5%; Pred. No. 0; Tridels 2:	; SEO ID NO 1 ; LENGTH: 2653 ; TYPE: DNA ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens	; CURRENT APPLICATION NUMBER: US/08/705,477E ; CURRENT FILING DATE: 1996-08-29 ; NUMBER OF SEQ ID NOS: 128 ; SOFTWARE: PatentIn version 3.1	APPLICANT: Overfelli, Ouathek APPLICANT: Pinto, John TITLE OF INVENTION: PROSTATE-SPECIFIC MEN FILE REFERENCE: 1769/41426-G	GENERAL INFORMATION: APPLICANT: Israeli, Rom APPLICANT: Heston, Wan APPLICANT: Fair, Will:	RESULT 3 US-08-705-477E-1 ; Sequence 1, Application US/08705477E ; Patent No. 6569432	2639	2579 G 1978 A	Db 2519 ATTCTTTAGAGAATCCGTATTGAAATTTGTGTGTGTATGTCACCAGAAAGAA	2459 1860	QY 1800 CTGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGG 1859
					0y 1		Qy 1 Db 1	Qy 1 Db 1	Qy 1 Db 1	Оу 1 рь 1	Oy 1 Db 1	Оу 1 Дь 1	Qy Db 1	Оу Дъ 1	Oy 1	Qy	Qy	Db 1:
99 TTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGAAGTGAAGAGACAGATTT			1610 GAGCATTATTGATCCATTAGGGTTACCAGACAGACCTTTTATAGGCATGTCTATG 1679	59 60	TTTCTGCAGTAAAAATTTTACAGAAATTGCTTCCAAGTTCAGCGAGAGACTCCAGGACT	1380 TCCCTTTTGATTGTCGAGATTATGCTGTAGTTTTAAGAAAGTATGCTGACAAATCTACA 1439	320 ACCTCACTGTGGCCCAGGTTCGAGGAGGATGGTGTTTGAGCTAGCCAATTCCATAGTGC 			1140 GCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAG 1199	1080 TITATGAAAGTTGGACTAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAA 1139 	1020 TGGTATACAACCTAACAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC 1079	960 ACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCT 1019	900 AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTG 959 	840 GAAGAACAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTG 899 	780 CTGTTGTTCATGAAACTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGG		1319 CAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA

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1560 TTGACAAAAGCAACCCAATATTGTTAAGAATGATGAATGA	480 CTGTTCATCCAGTTGGATACTATGATGCACAGAAGACTCCTAGAAAAAATGGGTGGCTCAG 539	Qy 4
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1440 ATATTTCTATGAAACATCCACAGGAAATGAAGACATACAGTTTATCATTTGATTCACTTT	TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCCAGGTTACC 41	
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1320 ACCTCACTGTGGCCCAGGTTCGAGGAGGGATGGTGTTTGAGCTAGCCAATTCCATAGTGC	AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG 29	Ωу 2
1260 ACAGTGTCTATGAAACATATGAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATC	Qy Query Match 84.5%; Score 1683.4; DB 4; Length 2387; Best Local Similarity 97.8%; Pred. No. 0; Matches 1717; Conservative 0; Mismatches 36; Indels 2; Gaps 1;	Query Ma Best Loc Matches
1200 GCAGAGCACGGTATACTAAAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC	LENGTH: 2387 Qy TYPE: LDN TYPE: LDN ORGANISM: Homo sapiens 8-705-477E-100 Db	; LENGTH: 2387 ; TYPE: DNA ; ORGANISM: HOMO US-08-705-477E-100
1140 GCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAG 	### QY Control	; CURRENT E ; NUMBER OF ; SOFTWARE: ; SEQ ID NO
1080 TTTATGAAAGTTGGACTAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAA 	APPLICANT: Pinto, John Qy TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF FILE REFERENCE: 1769/41426-G CURRENT APPLICATION NUMBER: US/08/705,477E Db	; APPLICA ; TITLE O ; FILE RE ; CURRENT
1020 TGGTATACAACCTAACAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC	Israeli, Ron S Heston, Warren D.W. Fair, William R. Db Overfelli, Onathok	; APPLICA ; APPLICA ; APPLICA
960 ACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCT 	OB-705-477E-100 Qy Sequence 100, Application US/08705477E Patent No. 6569432 GENERAL INFORMATION:	US-08-705-477E-100 Sequence 100, Ap Patent No. 65694 GENERAL INFORMAT
900 AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTG	39 AAAAAAAAAAAAAA 2653	Db 26
840 GAAGAACAATTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTG		Db 2579 Qy 1978
700 CIBILGITCA GAAAK IBIGAGGAGCTITGGAACAC TGAAAAANGGAAGGITGGAGACCTA 		Qy 1918
	ATTCTTTAGAGACTCTGTATTGAATTTGTGTGGTATGTCACTCAAAGAATAATGA 1917	<u>،</u> ب
	.800 CTGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGG 1859 Db	Qy 1

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RESULT 5
US-09-164-034B-1
; GENERAL INFORMATION:
; APPLICANT: Mincheff, Milcho S.
APPLICANT: Mincheff, Milcho S.
Toukinov, I. Dmitri
Touhak, Serguei
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Best Local Sim
Matches 1592;
                                                                                                                                                                       Local Similarity
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APPLICATION NUMBER: US/09/164,034B
FILING DATE: 30-Sep-1998
ATTORNEY/AGENT INFORMATION:
NAME: RAMSey, William S.
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                                                                                                                                                                                                                                                                                                                                                                       Ramsey, Cook, Looper & Kurlander, LI STREET: 10420 Little Patuxent Parkway, Suite 25 CITY: Columbia
STATE: Maryland
COUNTRY: USA
ZIP: 21044
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CORRESPONDENCE ADDRESS:
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TELEFAX: (410) 992-9540
ENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                   NAME: Ramsey, William S.
REGISTRATION NUMBER: 32,715
REFERENCE/DOCKET NUMBER: bril
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CURRENT APPLICATION NUMBER: US/08/705,477E
CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 97, Application US/08705477E
Patent No. 6569432
GENERAL INFORMATION:
APPLICANT: Israell, Ron S
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
APPLICANT: Overfelli, Ouathek
APPLICANT: Overfelli, Ouathek
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
 Sequence 96, Application US/08705477E Patent No. 6569432 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                              TAATGAGAAAAGGTTGAAGATAAAGTTCTGGTACTCATTTAAGTGTAATATTGAAAATTG
                                                                                                                                                                                              TAATGACAAAAGGTTGAAGATAAAGTTCTAGTACTCATTTAAGTGTAATATTGAAAATTG
                                                                                                                                                                                                                                           GAGCTTATAGTAGCAAAAAGAAAAGGAAATTCTATCCGAGATGTCCTTTGTTGTAGGCC
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96.2%;
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Pred. No. 3.4e-50;
0: Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 782;
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US-08-394-152A-45/c
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APPLICANT: Heston, Warren D.W.
APPLICANT: Heston, Walliam R.
APPLICANT: Fair, William R.
APPLICANT: Overfelli, Ouathek
APPLICANT: Overfelli, Ouathek
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
FILE REFERENCE: 1769/41426-G
CUCRENT APPLICATION NUMBER: US/08/705,477E
CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 96
LENGTH: 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5935818 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 230;
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Best Local :
                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
INFORMATION FOR
                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                            TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Heston, Warren D.W. APPLICANT: Fair, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                          ZIP: 10036
                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08394152A
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1185 Avenue of the Americas
               (212) 391-0525
                                                                                                                                                                                                                                                                                         United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ron S.
                                                                                                                                                                                                                                                                                          of America
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Pred. No. 3.4e-50;
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664 120 604 60 0;

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Mon Oct

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US-08-394-152A-45
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US-09-439-313-454/c
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                                                 ; TYPE: DNA; ORGANISM: Homo sapiens US-09-439-313-454
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Best Local S
Matches 256
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APPLICANT: Xu, Jian;
APPLICANT: Dillon,
APPLICANT: Mitcham,
                                                                                                                                                                                                                                                                                                                                                            Sequence 454, Application US/09439313 Patent No. 6329505
                                                                                     NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 454
LENGTH: 231
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 Matches
                        Query Match
                                                                                                                                       APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
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HYPOTHETICAL: I
ANTI-SENSE: NO
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LENGTH: 893 base pairs
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CLONE: Prostate Specific Membrane Antigen
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hes 256;
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STRANDEDNESS: doub
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             Local Similarity
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 222;
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                                                                                                                                                                                                                                                         Jiang Yuqui
Reed, Steven G.
Kalos, Michael
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Mitcham, Jennifer L.
Harlocker, Susan Louise
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Conservative
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E: Carcinoma
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NO
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92.8%;
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98.7%;
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             Score 220.2;
Pred. No. 2.9
 Mismatches
              .9e-49
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APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIA
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR
FILER REFERENCE: 210121.427C8
FULLE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 454
LENGTH: 231
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-352-616A-454/c
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; Patent No. 5538866
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US-08-325-553-27
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                          GENERAL INFORMATION:
          APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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Cooper & Dunham
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98.7%;
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Pred. No. 2.9e-49;
0; Mismatches 3
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                                                 MEMBRANE ANTIGEN
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; ANTI-SENSE: US-08-325-553-27
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Best Local Similarity
Matches 370; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 780 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
ATTORNEY_AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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TELEX: 422523 COOP UI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                               628 CAAGATGCACATCCACTCTACCAATGAAGGTGACGAGAATTTACAATGTGATAGGTACTCT
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                                          CTCAGACATAGTGAAAAACGAGGGCTACAAACCGAGGCGAAGCATCATCTTTGCTAGCTG
                                                                                CCCAGGAGTGGCTAAAGCTGGCACTGGAACTGCTATATTGTTGGAACTTGCCCGTGTGAT
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Pred. No. 1.8e-31;
0; Mismatches 342;
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                                                                                                                     Matches
                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
COMPUTER: IBM 330 46
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Israeli, Ron S. APPLICANT: Heston, Warren D APPLICANT: Fair, William R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                           448 AATTGCAGAGGCTGTTGGTCTTCCAAGTATTCCTGTTCATCCAGTTGGATACTATGATGC
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51.6%;
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of the
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                                                                                                                  Score 154.2; DB 2;
Pred. No. 1.8e-31;
0; Mismatches 342;
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APPLICANT: Heston, Warren D.W.

APPLICANT: Heston, Warren D.W.

APPLICANT: Heston, Warren D.W.

APPLICANT: Fair, William R.

APPLICANT: Pinto, John

TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND FILE REFERENCE: 1769/41426-G

CURRENT APPLICATION NUMBER: US/08/705,477E

CURRENT FILING DATE: 1996-08-29

NUMBER OF SEQ ID NOS: 128

SOFTWARE: Patentin version 3.1

SEQ ID NO 27

LENCTH: 780

TYPE: DNA

TYPE: DNA
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US-08-705-477E-27
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                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc_feature LOCATION: (196)..(197) OTHER INFORMATION: n=any
                                                                                  NAME/KEY: misc_feature LOCATION: (193)..(193)
                                                                                                                                     NAME/KEY: misc_feature LOCATION: (82)..(84) OTHER INFORMATION: n=any
                                                       FEATURE:
                                                                 OTHER INFORMATION: n=any
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; LOCATION: (721)...(724)
; OTHER INFORMATION: n=ar
US-08-705-477E-27
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Best Local :
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NAME/KEY: misc_feature
'COATION: (217)..(219)
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LOCATION: (263)..(263)
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Similarity 51.6%;
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 GCTGCATGCCAAAGCTTTCACTTACATCANNGCTTGGATGCTCCAGTCCTGGGAGCAAGC
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Pred. No. 1.8e-31;
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US-08-325-553-28
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                                                                                                                                                                              Matches
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                          TOPOLOGY: Li
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
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APPLICATION NUMBER: US/07/973,337A
FILING DATE: 05 NOV 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                              HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 664-05
TELEX: 422523 COOP UI
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                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                         149 GGCGTTATTAAAGGCTATGAGGAACCAGACCGCTACATTGTAGTAGGAGCCCAGAGAGAC
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Fair, William R.
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                                                                                                                                                                        Score 85.8; DI
Pred. No. 2.6e
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2.6e-13;
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Query Match
Best Local Similarity
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RESULT 15
US-08-394-152A-28
US-08-394-152A-28
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                                                                                                                                                   TELEPHONE: (212) 278-0
TELEFAX: (212) 391-052
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PROSTAGE TITLE OF INVENTION: USES THEREOF
                     HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM 330
OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 24-FEE CLASSIFICATION: 435
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                                                                            TOPOLOGY:
                                                                                                 STRANDEDNESS: double
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1185 Avenue of the Americas
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ON: 435
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4.3%;

Score Pred.

85.8; DB 2; No. 2.6e-13;

Length 660;

Matches	267; Conservative 0; Mismatches 218; Indels 10; Gaps 5;
Qy	620 CAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGATA 679
рb	89 CAAAATGTGAAGCTCACTGTGAACAATGTACTGAAAGAAA
Qy	680 GGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTCACCGGGAC 739
Db	149 GGCGTTATTAAAGGCTATGAGGAACCAGACCGCTACATTGTAGTAGGAGCCCAGAGAGAC 208
Qy	740 TCATGGGTGTTTGGTGGTATTGACCCTCAGAGT-GGAGCAGCTGTTGTTCATGAAACTGT 798
Вb	209 GCTTGGGGCCCTGGTNGTTGCGAAGTCCAGTGTGGGAACAGGTCTTNCTGTTGAAACTTG 268
Qy	799 GAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAACAATTTTGT 854
Db	269 CCCAAGTATTCTCAGATATGATTTCAAAAGATGGATTTAGACCCAGCAGGAGTATTATCT 328
ОУ	855 TTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCAGAGG 911
Db	329 TTGCCAGCTGGACTGCAGGAGACTATGGAGCTGTTGGTCCGACTGAGTGGCTGGAGGGGT 388
Qy	912 ATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTATAG 971
DЪ	389 ACCTTTCATCTTTGCATCTAAAGNNNGCTTTCACTTACATTAATNCTGGATAAAGTCGTC 448
Qy	972 AAGGAAACTA-CACTCTGAGAGTTGATTGTACACCACTGATGTACAGCTTGGTATACAAC 1030
Db	449 CTGGGTACTAGCAACTTCAAGGTTTCTGCCAGCCCCCTATTATATACACTTATGGGGAAG 508
Qy	1031 CTAACAAAAGAGCTGAAAAGC-CCTGATGAAGGCTTTGAAGGCAAATCTCTTTTATGAAAG 1089
Db	509 ATAATGCAGGANNCGTAAAGCATCCGANNNNNNNNTTGATGGAAAATATCTATATCGAAA 568
Qy	1090 TTGGACTAAAAAAAG 1104
Db	569 CAGTAATTGGATTAG 583
Search cou Job time	Search completed: October 4, 2003, 20:58:28 Job time : 182 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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          October 4, 2003, 19:30:56; Search time 649 Seconds (without alignments) 7829.460 Million cell upda
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Copyright (c) 1993 - 2003 Compu
                                                                                                                                                             /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	BIG	ID	Description
1	1702.6	85.5	2653	10	US-09-969-708-536	Sequence 536, Ar
2	1702.6	85.5	2653	12	US-09-873-319-451	Sequence 451, App
ω		85.5	2653	12	US-09-960-706-716	71
4	1702.6	85.5	2653	12	US-10-210-120-5	رن د
5		85.5	2653	14	US-10-094-699-2	N.
σ	1702.6	85.5	2653	14	US-10-205-823-131	131
7	1687.2	84.7	2558	10	US-09-978-295A-617	617,
8	1687.2	84.7	2558	10	US-09-978-697-617	617,
9	1687.2	84.7	2558	10	US-09-978-192A-617	617,
10	1687.2	84.7	2558	10	US-09-999-832A-617	617
11	1687.2	84.7	2558	11	US-09-978-189-617	617,
12	1687.2	84.7	2558	11	US-09-978-608A-617	617,
13	1687.2	84.7	2558	11	US-09-978-585A-617	617,
14	1687.2	84.7	2558	11	US-09-978-191A-617	617,
15	1687.2	84.7	2558	11	US-09-978-403A-617	
16	1687.2	84.7	3772	_	110-00-070-5643-617	7.7

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18
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-10-17	-10-17	-10-17	US-10-173-691-103	-10-17	-10-17	US-10-196-747-103	-10 - 18	US-10-145-128A-617	-10-19	-10 - 18	-10 - 19	US-10-143-030A-617	-10-01	US-10-002-967A-617	US-10-143-031A-617	US-09-978-298A-617	US-09-978-188A-617	US-09-978-375A-617	US-09-978-643A-617	US-09-978-187B-617	US-09-978-757A-617	US-09-999-830A-617	US-09-978-193A-617	US-09-978-423A-617	US-09-918-585A-617	-824-	US-09-981-915A-617
Sequence 103,			Sequence 103,			Sequence 103,																			Sequence 617,		Sequence 617,
App	Αp	Ą	Ąp	Ąρ	Αp	Αp	Ąp	Ąρ	Αp	Αp	Αp	Αp	Ąρ	Αp	Αp	Αþ	Ą	Ą	Ą	Αþ	Ą	Ą	Ą	Ą	Ą	Ą	Αp

ALIGNMENTS

US-09-969-708-536

Sequence 536, Application US/09969708 Patent No. US20020102532A1

20 В Qγ В 8 ; TYPE: DNA; ORGANISM: Homosapiens US-09-969-708-536 Query Match Best Local Similarity Matches 1729; Conserv NUMBER OF SEQ ID NOS: 658
SOFTWARE: PatentIn version 3.0
SEQ ID NO 536
LENGTH: 2653 GENERAL INFORMATION:
APPLICANT: Augustus, Meena CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03 TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign TITLE OF INVENTION: Sets FILE REFERENCE: 689290-70 PRIOR APPLICATION NUMBER: US/60/237,425 PRIOR FILING DATE: 2000-10-03 899 360 300 ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTG 240 AGGTTAAAAATGCCCAGCTGGCAGGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCCAGGTTACC AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCCGACCCTGCTG ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGATGGTTGGAATCTTCCTGGAGGTGGTG Conservative 98.5%; 0; Score 1702.6; Pred. No. 0; Mismatches DB 10; 24; Indels Length 2653; 2; Gaps 1018 359 958

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APPLICANT: Getzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Yamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Hyperplasia Using Gene Ex
FILE REFERENCE: 44921-509-US
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT FILING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 451
LENGTH: 2653
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US-09-873-319-451
US-09-873-319-451, Application US/09873319A
Sequence 451, Application US/09873319A
                                                                                                         ; OTHER INFORMATION: US-09-873-319-451
                                                   Query Match
Best Local Similarity
Matches 1729; Conserv
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                                                                                                                                  TYPE: DNA
ORGANISM: Homo :
FEATURE:
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Pred. No. 0;
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                                                                                                 TITLE OF INVENTION: Identifying Drugs for and Dia TITLE OF INVENTION: Gene Expression Profiles FILE REFERENCE: 4491-5029-01US

CURRENT APPLICATION NUMBER: US/09/960,706

CURRENT FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 60/23,323

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 09/873,319

PRIOR FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 1124

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 716

LENGTH: 2653

TYPE: DNA

ORGANIEM: Homo sapiens
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Publication No. US2003013421
GENERAL INFORMATION:
APPLICANT: Munger, William
             Matches
                        Query Match
Best Local Similarity
                                                                OTHER INFORMATION: -09-960-706-716
                                                                                                                                                                                                                                                                                                                                                           -09-960-706-716
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Pred. No. 0;
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                                   ACAGTGTCTATGAAACATATGAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATC
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                                                             SOFTWARE: PatentIn
SEQ ID NO 5
LENGTH: 2653
Query Match
                                                                                                 PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
                                                                                                                                      APPLICANT: Sreekumar, Arun
TITLE OF INVENTION: Expression Profile of
EILE REFERENCE: UM-07221
CURRENT APPLICATION NUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
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                                                TYPE: DN
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                 Sequence 2, Application US/10094699
PUDDICATION NO. US20030046714A1
GENERAL INFORMATION:
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: DIAMOND, David, C.
TITLE OF INVENTION: CANCER
FILE REFERENCE: CTLIMM.015A
CURRENT APPLICATION NUMBER: US/10/094,699
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/274,063
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 2
LENGTH: 2653
TYPE: DNA
ORGANISM: Homo sapien
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RESULT 6

US-10-205-823-131

Sequence 131, Application US/10205823

Publication No. US20030108963A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.

APPLICANT: Endege, Wilson O.

APPLICANT: Gannavarapu, Manjula

APPLICANT: Gorbatcheva, Bella

APPLICANT: Hoersch, Sebastian

APPLICANT: Hoersch, Sebastian

APPLICANT: Wonsey, Angela M.

APPLICANT: Schaet, Shubhangi

APPLICANT: Anderson, Dustin

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

FILE REFERENCE: MRI-044

CURRENT APPLICATION NUMBER: US/10/205,823
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OR APPLICATION NUMBER: 60/307,982
OR FILING DATE: 2001-07-25
OR APPLICATION NUMBER: 60/314,356
OR FILING DATE: 2001-08-22
OR APPLICATION NUMBER: 60/325,020
OR APPLICATION NUMBER: 60/325,020
OR FILING DATE: 2001-09-25
OR APPLICATION NUMBER: 60/341,746
OR FILING DATE: 2001-12-12
COR APPLICATION NUMBER: 60/362,158
COR FILING DATE: 2002-03-05
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Sequence
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
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CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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LOR APPLICATION NUMBER: 60/07-
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R APPLICATION NUMBER: 60/07
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APPLICATION 1
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Tumas, Daniel
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Grimaldi, J. Christopher
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APPLICATION NUMBER: 60/081817 60/081952 60/081819

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                      APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transme
TITLE OF INVENTION: Acids Encoding the
TITLE OF INVENTION: Acids Encoding the
TILE REFERENCE: P2630P1C27
CURRENT APPLICATION NUMBER: US/09/978,69
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Bernyers, Luc
APPLICANT: Beton, Dan
APPLICANT: Ferrara, Napole
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                                                                                                     Sequence 617, Application Patent No. US20020177553A1 GENERAL INFORMATION:
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: Botstein, David
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                                                 APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, Daniel
APPLICANT: Williams, D. Mickey
APPLICANT: Williams, D. Mickey
APPLICANT: Wood, Williams I.
TITLE OF INVENTION: Secreted and Transmembran
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas
Roy, Margaret Ar
Shelton, David I
Stewart, Timothy
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Fong, Sherm
Gao, Wei-Qi
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Gerritsen,
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Godowski, Paul J.
Grimaldi, J. Christopher
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GENERAL INFORMATION:
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APPLICANT: Baker Kevin P.
APPLICANT: Baker Kevin P.
APPLICANT: Betstein, David
APPLICANT: Eston, Dan
APPLICANT: Eston, Dan
APPLICANT: Eston, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Geodard, Audrey
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Mayori, Ivar J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Paoni, Vicholas F.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Wood, William J.
APPLICANT: Wood, William S.
APPLICANT: Wood, William S.
APPLICANT: Wood, William J.
APPLICANTON NUMBER: 00/01-10-24
PRIOR APPLICATION NUMBER: 00/05250
PRIOR TILING DATE: 1997-11-03
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Ashkenazi, Avi Baker Kevin P. Botstein, David Ashkenazi,

Eaton, Desnoyers, Luc

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Ferrara, Napoleon
Filvaroff, Ellen
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qlang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.

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TITLE OF INVENTION: Secreted and Tra
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2630P1C7
       DR APPLICATION NUMBER: 60,77791
DR FILING DATE: 1998-03-12
DR APPLICATION NUMBER: 60,7078004
DR FILING DATE: 1998-03-13
DR APPLICATION NUMBER: 60,7078086
DR FILING DATE: 1998-03-20
DR APPLICATION NUMBER: 60,7078936
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DR APPLICATION NUMBER: 60,7078939
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DR APPLICATION NUMBER: 60,7079923
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OR APPLICATION NUMBER: 60/065364
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OR APPLICATION NUMBER: 60/077450
OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/077632
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OR FILING DATE: 1998-04-01
OR FILING DATE: 1998-04-08
OR APPLICATION NUMBER: 60/081049
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OR APPLICATION NUMBER: 60/081195
OR APPLICATION NUMBER: 60/081203
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OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081229
OR APPLICATION NUMBER: 60/08125
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081817
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OR FILING DATE: 1998-04-15
OR FILING DATE: 1998-04-21
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
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AGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	1121 CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTG 600 TTACTGGAAACTTTTCTACACACAAAAGTCCAGATGCACATCCACTCTACCA 11111111111111111111111	-G &-8	420 CAGCAAATGAATACGCTTATAGGCATGGAATGCAAGAGGCTGTTGGTCTTCCAAGTATTC 4 1011 1 1 1 1 1 1 1 1 1	881 A 360 T	- G 88	Query Match 84.7%; Score 1687.2; DB 11; Length 2558; Best Local Similarity 98.6%; Pred. No. 0; Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1; Qy 240 AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTAGTCAGACCCTGCTG 299	; PRIOR APPLICATION NUMBER: 00/0037/3 ; PRIOR FILING DATE: 1998-05-15 ; PRIOR APPLICATION NUMBER: 60/085704 ; PRIOR FILING DATE: 1998-05-15 ; PRIOR APPLICATION NUMBER: 60/085697	5-15 5-15	APPLICATION NUMBER: 60, FILING DATE: 1998-05-11 APPLICATION NUMBER: 60, FILING DATE: 1998-05-11	APPLICATION NUMBER: 60/0853 FILLING DATE: 1998-05-13 APPLICATION NUMBER: 60/0855 FILLING DATE: 1998-05-15	APPLICATION FILING DATE APPLICATION FILING DATE	NUMBER: 60/08462 : 1998-05-07 : NUMBER: 60/08464 : 1998-05-07	APPLICATION NUMBER: 60/0845 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/0846 FILING DATE: 1998-5-07	APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0	RIOR FILING DATE: 1998-0 RIOR APPLICATION NUMBER: RIOR FILING DATE: 1998-0
QY 1740 TIGATATIGAAAGCAAAGTIGACCCTTCCAAGGCCTGGGGAGATGTGAAGAGACAGATTT 1799		Db 2141 TIĞACAAAACCAACTAGTATTAAĞAATĞATĞATĞATĞATĞATGAACTATGTTTCTGĞAAA 2200 2141 TIĞACAAAACCAATAĞTATTAAĞAATĞATĞATĞATĞATĞATĞATĞATCTATĞ 1679 Qy 1620 GAĞCATTTATTĞATCCATTAĞĞĞTTACCAĞACAĞACCTTTTTATAĞĞCATĞTCATCTATĞ 1679	Qy 1500 TITCTGCAGTAAAAATTTTACAGAAATTGCTTCCAAGTTCAGGAGACTCCAGGACT 1559		0 TCCCTTTTGATTGTCGAGATTATGCTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACA 	1200 ACMUTETE LA DAMACKATATIONE LE CONTROLLE	1200 1781	QY 1140 GCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAG 1199 	QY 1080 TTTATGAAAGTTGGACTAAAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAA 1139	QY 1020 TGGTATACAACCTAACAAAAGAGCTGAAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC 1079	QY 960 ACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCT 1019	QY 900 AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGGCGTGGCGTGATATATAATGCTG 959	QY 840 GAAGAACAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTGGTTCTACTG 899	QY 780 CTGTTGTTCATGAAACTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGG	QY 720 TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG 779

OY 360 TCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTACC 419	QY 300 ACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCTGGAGGTGGTG 359	QY 240 AGGTTAAAAATGCCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCAGACCCTGCTG 299	Query Match 84.7%; Score 1687.2; DB 11; Length 2558; Best Local Similarity 98.6%; Pred. No. 0; Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;		סי ט	TITLE OF INVENTICE TITLE OF INVENTICE FILE REFERENCE: FILE REFERENCE: FILE REFERENCE FILE REPELICATION OF THE PROPERTY APPLICATION OF THE PROPERTY APPLICATION OF THE PROPERTY APPLICATION OF THE PROPERTY APPLICATION OF T	APPLICANT: Stewart, APPLICANT: Tumas, Da APPLICANT: Williams, APPLICANT: Wood, Wil	APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT:	APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul (APPLICANT: Grimaldi, J. Ch APPLICANT: Gurney, Austin 1	•• •• •• ••	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	GENERAL INFOR APPLICANT: A APPLICANT: I APPLICANT: I	RESULT 12 US-09-978-608A-617 ; Sequence 617, Application US/09978608A ; Publication No. US20030045462A1	QY 1918 GTATATTGATAAATTTTAAAATTGGTATATTTGAAATAAAGTTGAATATATAAAT 1975	2441 ATTTTTAGAGAATCCGTATTGAATTTGTGTGTGTCACTCAGAAAGAA	
	Db Db	ДУ Db	Фр	Qу	Qy Db	Qy	Qy	Qy	Qy Db	QУ	Qy	Qγ	Qy	Qy	Qy	Db Qy	Qy Db
1440 ATATTTCTATGAAACATCCACAGGAAATGAAGACATTACATTTATCATTTCACTTT 1499	TCCCTTTTGATTGTCGAGATARGCTGTAGTTTTAAGAAAGTCTACA	ACCTCACTGTGGCCCAGGTTCGAGGAGGGATGGTGTTTGAGCTAATTCCATAGTGG	ACAGTGTCTATGAAACATATGAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATC	1200 GCAGAGCACGGTATACTAAAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC 1259 	1140 GCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAG 1199	1080 TITATGAAAGTIGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAA 1139 	1020 TGGTATACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTC 1079 	960 ACTCATCTATAGAAGGAAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCT 1019 	900 AGTGGGCAGAGGATAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTG 959 	840 GAAGAACAATTTTGTTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTG 899 	780 CTGTTGTTCATGAAACTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGG	720 TTCTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAG 779	660 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	600 TTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATGCACTCTACCAATGAAGTGA 659 	CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCCTACAATGTTGGACCTGGCT	480 CTGTTCATCCAGTTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAG 539	420 CAGCAAATGAATACGCTTATAGGCATGGAATTGCAGAGGCTGTTGGTCCTTCCAAGTATTC 479

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Sequence 617, Application US/0997;
Sequence 617, Application US/0997;
Publication No. US20030049633A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Girmaldi, J. Christopl
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
                                                             APPLICANT: Shelton, David I
APPLICANT: Stewart, Timothy
APPLICANT: Timas, Daniel
APPLICANT: Williams, P. Mic
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted
TITLE OF INVENTION: ACIDS E
FILE REFERENCE: P2630P1C15
Prior Application removed
SEQ ID NO 617
LENGTH: 2558
                                         CURRENT APPLICATION NUMBER: US/09/978
CURRENT FILING DATE: 2001-10-16
                               NUMBER OF SEQ ID NOS: 624
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                                                                                      T: Wood, William I.
INVENTION: Secreted and
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Grinaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Williams, P. Mickey
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Stewart, Timothy A.
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 GCAGAGCACGGTATACTAAAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Botstein, David
Desnoyers, Luc
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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
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Shelton, David L.
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Kuo, Sophia S.
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APPLICANT: Wood, William I.
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Gerber, Hanspeter
Geritsen, Mary E.
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Filvaroff, Ellen
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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Botstein, David
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Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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ALIGNMENTS

RESULT 1 US-09-822-827-944

Sequence 944, Application US/09822827 Patent No. US20020081680A1 GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822,827 CURRENT FILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 982 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 944 LENGTH: 750

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APPLICANT: Baker Kevin P
APPLICANT: Botstein, Dav
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                     Tumas, Daniel
Williams, P. Mickey
Wood, William I.
                                                   Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                       Gao,
                                                                                                                                Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
                                                                                                                                                                                      Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
                                                                                     Paoni, Nicholas F
                                                                                                  Pan, James;
                                                                                                          Napier, Mary A.
                                                                                                                                                                 Godowski, Paul J.
Grimaldi, J. Christopher
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Filvaroff,
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                                                                                                                     Sophia S.
                                                                                                                                                                                                                      Wei-Qiang
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ff, Ellen
           Secreted and
 Acids Encoding
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           Transmembrane Polypeptides
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PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081203
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PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-15
PRIOR PPLICATION NUMBER: 60/081955
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PRIOR PPLICATION NUMBER: 60/081952
PRIOR PPLICATION NUMBER: 60/082568
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PRIOR PPLICATION NUMBER: 60/082569
PRIOR PPLICATION NUMBER: 60/082804
PRIOR PILLING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082704
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PRIOR PPLICATION NUMBER: 60/084414
PRIOR PPLICATION NUMBER: 60/08459
PRIOR PPLICATION NUMBER: 60/084640
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RESULT 4
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; Patent No. US20020177553A1
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Forrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580
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FILING DATE: 1998-05-15
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                                                                                                INFORMATION:
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          Eaton, Dan
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Filvaroff, Ellen
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
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OR APPLICATION NUMBER: 60/078939
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
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FILING DATE: 1998-03-1
APPLICATION NUMBER: 60
FILING DATE: 1998-03-1
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FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/
FILING DATE: 1997-11-21
APPLICATION NUMBER: FILING DATE: 1998-0:
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FILING DATE: 1998-03-12
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                                                  APPLICATION NUMBER:
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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Goddard, Audrey
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                                     DKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMNDQL
MFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDV
                                                                          EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSG
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RESULT 5
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077632
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CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION UNMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Williams, P. Mickey
Wood, William I.
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Grimaldi, J. Christopher
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Hillan, Kenneth J
Kljavin, Ivar J.
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PR APPLICATION NUMBER: 60/082569

R FILING DATE: 1998-04-21

R APPLICATION NUMBER: 60/082704

DR FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082804
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DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081817
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081819
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081952
DR FILING DATE: 1998-04-15
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DR APPLICATION NUMBER: 60/081070

DR FILING DATE: 1998-04-08

DR APPLICATION NUMBER: 60/081049

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DR FILING DATE: 1998-04-09

DR APPLICATION NUMBER: 60/081203

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DR FILING DATE: 1998-04-09

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OR APPLICATION NUMBER: 60/080165

OR FILING DATE: 1998-03-31

OR APPLICATION NUMBER: 60/080194

OR FILING DATE: 1998-03-31

OR APPLICATION NUMBER: 60/080327

OR FILING DATE: 1998-04-01

OR APPLICATION NUMBER: 60/080328

OR APPLICATION NUMBER: 60/080328
                APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
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APPLICATION NUMBER: 60
FILING DATE: 1998-04-
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APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/079923
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/084366
FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
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APPLICATION UNMBER: 60/083558
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Pred. No. 7.3e-217;
6; Mismatches 3;
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; SOFTWARE: FastSEQ i
SEQ ID NO 944
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Publication N
                                                                                     APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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Query Match
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Vedvick, Thomas S
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Vinals de Bassols, Carlota
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Hepler, William T.
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RESULT 7
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CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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                                                                         TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C7
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Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Grinaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Baker Kevin P.
Botstein, David
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Shelton, David L.
Stewart, Timothy A.
                                                                                                                    Wood,
                                                                                                                                Tumas, Daniel
Williams, P. Mickey
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Napier, Mary A.
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                                                                                                                    William I.
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           APPLICATION NUMBER: 60/081203
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 Godowski,
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Baker Kevin P.
                   Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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APPLICATION NUMBER: 60/083742 FILING DATE: 1998-04-30

APPLICATION NUMBER: 60/084366

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1998-05-07

APPLICATION NUMBER: 60/084643 FILING DATE: 1998-05-07

APPLICATION NUMBER: 60/085339

1998-05-1

60/085338

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RESULT 9
US-09-78-585A-618
Sequence 618, Application US/09978585A
Publication No. US20030049633A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Botsoyers, Luc
APPLICANT: Eaton, Dan
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LENGTH: 750
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Best Local
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/978,608A CURRENT FILING DATE: 2001-10-16 NUMBER OF SEQ ID NOS: 624
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Roy, Margaret Ann
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Hillan, Kenneth
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Pred. No. 7.3e-217;
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SEQ ID NO 618
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APPLICANT: Wood, William 1.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT APPLICATION DATE: 2001-10-16
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                       KRQISVAAFTVQAAAETLSEVA 442
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                                                                                                                   DKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMNDQL
KRQIYVAAFTVQAAAETLSEVA
                                                 MFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEV
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Godowski, Paul J.
Grimaldi, J. Christopher
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Gao, Wei-Qiang
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Stewart, Timothy A.
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Pred. No. 7.3e-217;
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CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
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APPLICANT: Baker Kevin P
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                                                                              APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
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FILING DATE: 1998-03-10
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                                 APPLICATION NUMBER: 60/0
FILING DATE: 1998-03-26
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FILING DATE: 1998-03-12
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Botstein, David
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PRIOR OR APPLICATION NUMBER: 60/082568
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OR FILING DATE: 1998-04-01 DR FILING DATE: 1998-03-27

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/91858
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066364
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Williams, P. Mickey
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Shelton, David L.
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Grimaldi, J. Christopher
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Kuo, Sophia S.
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Desnoyers, Luc
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APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/080107

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PRIOR FILING DATE: 1998-03-31

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PRIOR APPLICATION NUMBER: 60/080328

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PRIOR FILING DATE: 1998-04-01

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PRIOR PRIOR APPLICATION NUMBER: 60/080333

PRIOR APPLICATION NUMBER: 60/080334

PRIOR APPLICATION NUMBER: 60/081070

PRIOR APPLICATION NUMBER: 60/081070

PRIOR PRILING DATE: 1998-04-08

PRIOR PILING DATE: 1998-04-08

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PRIOR APPLICATION NUMBER: 60/081195

PRIOR APPLICATION NUMBER: 60/081203

PRIOR APPLICATION NUMBER: 60/081229

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PRIOR APPLICATION NUMBER: 60/081259

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PRIOR APPLICATION NUMBER: 60/081955

PRIOR APPLICATION NUMBER: 60/081956

PRIOR ETLING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079664
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PRIOR ETLING DATE: 1998-03-27
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PRIOR PRILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
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PRIOR APPLICATION NUMBER: 60/079728
PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR APPLICATION NUMBER: 60/080105
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DR FILING DATE: 1998-03-13
DR APPLICATION NUMBER: 60/078886
DR APPLICATION NUMBER: 60/078936
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DR FILING DATE: 1998-03-20
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DR APPLICATION NUMBER: 60/078939
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DR FILING DATE: 1998-03-25
DR FILING DATE: 1998-03-26
DR APPLICATION NUMBER: 60/079664
DR APPLICATION NUMBER: 60/079669
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079663
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RESULT 12
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin |
APPLICANT: Baker, Nevin |
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                           Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                             Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Gerritsen, Mary E.
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Botstein, David
           Tumas, Da
Williams,
                                                                                                                                                         Goddard, Audrey
                                                                                                                                                                                                                                    Eaton,
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b. US20030050241A1
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OR FILING DATE: 1998-03-25

OR APPLICATION NUMBER: 60/079656

OR FILING DATE: 1998-03-26

COR APPLICATION NUMBER: 60/079664

COR APPLICATION NUMBER: 60/079669
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OR FILING DATE: 1998-03-27
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OR APPLICATION NUMBER: 60/080107
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OR APPLICATION NUMBER: 60/078886
OR FILING DATE: 1998-03-20
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OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079939
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OR APPLICATION NUMBER: 60/080194

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OR APPLICATION NUMBER: 60/080327

OR FILING DATE: 1998-04-01

OR APPLICATION NUMBER: 60/080328

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DR APPLICATION NUMBER: 60/079689
DR FILING DATE: 1998-03-27
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OR APPLICATION NUMBER: 60/00
OR FILING DATE: 1997-11-13
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FILING DATE: 2001-07-30
APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/077791
FILING DATE: 1998-03-12
APPLICATION NUMBER: 60/078004
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NUMBER: 60/
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RESULT 13
US-09-999-833A-618
Sequence 618, Application US/09999833A
PUBLICATION NO. US20030054405A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
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Best Local S
Matches 433
APPLICANT:
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APPLICATION NUMBER: 60/083558 FILING DATE: 1998-04-29

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1998-04-29

60/083559

DR APPLICATION NUMBER: 60/083495
DR FILING DATE: 1998-04-29
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083496
DR FILING DATE: 1998-04-29
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DR APPLICATION NUMBER: 60/083545
DR FILING DATE: 1998-04-29
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1998-04-29

60/083392

APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-27

OR APPLICATION NUMBER: 60/082700
R FILLING DATE: 1998-04-22
R PRICATION NUMBER: 60/082797
R FILLING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/82796
R FILING DATE: 1998-04-23

FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-22

60/082804

APPLICATION NUMBER: 60/ FILING DATE: 1998-04-21

60/082569

APPLICATION NUMBER: 60/082704

FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21

FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15

APPLICATION NUMBER: 60/081952

APPLICATION NUMBER: 60/ FILING DATE: 1998-04-09

60/081229

APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09

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NUMBER: 60/ : 1998-04-08 1998-04-08

60/081195 60/081071

APPLICATION NUMBER: 60 FILING DATE: 1998-04-1

APPLICATION NUMBER:

60/081817 60/081955

DR APPLICATION NUMBER: 60/083500

R FILLING DATE: 1998-04-29

PR APPLICATION NUMBER: 60/083742

DR FILLING DATE: 1998-04-30

DR APPLICATION NUMBER: 60/084366

DR FILLING DATE: 1998-05-05

DR APPLICATION NUMBER: 60/084414

DR FILLING DATE: 1998-05-06

DR APPLICATION NUMBER: 60/084441

DR APPLICATION NUMBER: 60/084441

DR APPLICATION NUMBER: 60/084441

PR APPLICATION NUMBER: 60/084639
PR FILING DATE: 1998-05-07
PR APPLICATION NUMBER: 60/084640
PR FILING DATE: 1998-05-07
PR APPLICATION NUMBER: 60/084598
PR FILING DATE: 1998-05-07
PR APPLICATION NUMBER: 60/084600
PR APPLICATION NUMBER: 60/084600

FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084637
FILING DATE: 1998-05-07

FILING DATE APPLICATION

1998-05-07

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CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062249
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
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DR FILING DATE: 1998-03-10
DR APPLICATION NUMBER: 60/077632
DR FILING DATE: 1998-03-11
DR APPLICATION NUMBER: 60/077641
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/077791
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APPLICATION NUMBER: 60/078004
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Grimaldi, J. Christopher
Gurney, Austin L.
Gullan, Kenneth J
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                                                          NUMBER: 60/079786: 1998-03-27
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RESULT 14
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C12
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OR APPLICATION NUMBER: 60/066364
OR FILING DATE: 1997-11-21
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OR APPLICATION NUMBER: 60/077450
OR FILING DATE: 1998-03-10
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Baker Kevin P.
Botstein, David
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Shelton, David L.
Stewart, Timothy A.
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Gurney, Austin L.
Hillan, Kenneth J
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Gerritsen, Mary E
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Kuo, Sophia S.
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                                                                                                 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C14
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       PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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CURRENT FILING DATE: 2001-10-17
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                                                                                                                                             Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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Botstein, David
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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APPLICATION NUMBER: 60/078939
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APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/080165
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FILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/084366
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APPLICATION NUMBER: 60/082804
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Maximum Match 100%
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1: /cgn2_6/ptodata/2

2: /cgn2_6/ptodata/2

3: /cgn2_6/ptodata/2

4: /cgn2_6/ptodata/2

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Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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PCT-US95-11720-18
US-08-325-553-2
US-08-394-152A-2
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US-08-957-940-1
US-08-547-197-1
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US-09-446-553-11
US-08-335-553-11
US-08-335-553-11
US-08-335-477E-11
US-08-335-477E-11
US-08-335-553-71
US-09-634-238-271
US-09-634-238-271
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US-08-528-122-18
Sequence 18, Application US/08528122
; Patent No. 5726044
  Query Match
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APPLICANT: LO, KIN-MING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LO, KIN-MING
APPLICANT: SUDO, YUKIO
APPLICANT: GILLIES, STEPHEN D.
APPLICANT: GILLIES, STEPHEN D.
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY
TITLE OF INVENTION: PROTEINS AS IMMUNOFUSINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 20
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT
                                                                                                                                                   FEATURE:
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91	91	91.5	93.5	93.5	93.5	94	94.5	94.5	94.5	95.5	95.5	96	96	96.5	96.5	96.5	96.5
3.9	3.9	3.9	4.0	4.0	4.0	4.0	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1
514	514	1151	2233	2233	2233	727	956	354	328	981	597	396	396	377	377	377	377
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Sequence 2, Appli	Sequence 2, Appli	Sequence 3242, Ap	Sequence 1, Appli	N	Sequence 1, Appli	Sequence 4067, Ap	Sequence 5007, Ap	Sequence 5179, Ap	Sequence 3229, Ap	Sequence 2, Appli	Sequence 32073, A	Sequence 2, Appli	-	•	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli

ALIGNMENTS

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/528,122
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEPAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 707 amino acids
TYPE: amino acid
                                                      NAME/KEY: Protein LOCATION: 1..707 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                    MOLECULE TYPE: protein
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COUNTRY: US
ZIP: 02110
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TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: FI
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Matches
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                                     TELEFAX: 617-248-7100 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EXTITLE OF INVENTION: PR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                              REGISTRATION UMBER: 27,829
REFERENCE/DOCKET NUMBER: FI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           STREET: 125
CITY: BOSTO
STATE: MA
COUNTRY: US
ZIP: 02110
                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
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ADDRESSEE: THIBEAU
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                        LENGTH:
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US-08-325-553-2
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                                                                                                                                                                                                                                                                                                                     Sequence 2,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Israel
                                                               COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                    APPLICANT: Fair, Wil
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              APPLICANT:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                STREET: 30 Rock
CITY: New York
STATE: New York
CLASSIFICATION:
                           FILING DATE:
                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                  Sequence 2, Application US/08394152A Patent No. 5935818 GENERAL INFORMATION:
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Best Local :
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELEFHONE: (212) 977-9550
TELEFHONE: (212) 977-9550
TELEFAX: (212) 664-0525
                                                                     APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECII
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
STREET: 1185 AVE
CITY: New York
STATE: New York
COUNTRY: United
ZIP: 10036
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              of America
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Pred. No. 1.8e-214;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LENGTH: 750 amino acids
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/394,152A FILING DATE: 24-FEB-95
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                                                         KRQIYVAAFTVQAAAETLSEVA
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Pred. No. 1.8e-214;
6; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: Murphy, Gerald P.
APPLICANT: Holmes, Eric H.
APPLICANT: Holmes, Eric H.
APPLICANT: Tino, William Thomas
APPLICANT: TINCE OF INVENTION: MONOCLONAL AND TITLE OF INVENTION: MEMBRANE ANTIC

MONOCLONAL ANTIBODIES SPECIFIC FOR THE EXTRACELLULAR DOMAIN OF PROSTATE-SPECIFIC

MEMBRANE ANTIGEN

Sequence 2 Patent No.

2, Application 5. 6150508

US/09044668

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Best Local S
Matches 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Baldwin, Geraldine F
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 8511
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & E
STREET: 1155 Avenue o
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: lir
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KRQIYVAAFTVQAAAETLSEVA
                         KRQISVAAFTVQAAAETLSEVA 442
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1155 Avenue of the Americas
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llarity 98.0%;
Conservative
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Pred. No. 1.8e-214;
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                                                                                                              Sequence 101, Application Patent No. 6569432 GENERAL INFORMATION:
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CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 750
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANY: Israeli, Ron S
APPLICANY: Heston, Warren D.W.
APPLICANT: Fair, William R.
APPLICANT: Overfelli, Ouathek
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
FILE REFERENCE: 1769/41426-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Applic Patent No. 6569432
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Best Local
APPLICANT: Pinto, John
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE
FILE REFERENCE: 1769/41426-G
CURRENT APPLICATION NUMBER: US/08/705,477E
                                                          APPLICANT:
                                                                                    APPLICANT: Israeli, APPLICANT: Heston,
                                                                                                                                                                                                           729
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                                                                                                                                                                                                                                                                          KRQISVAAFTVQAAAETLSEVA 442
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                                                          Fair, William
Overfelli, Oua
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98.0%;
                                                           Ouathek
                                                                                                                                          US/08705477E
                                                                                     D.W.
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Pred. No. 1.8e-214;
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; SOFTWARE: PatentIn versic
; SEQ ID NO 101
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-705-477E-101
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Best Local Similarity
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                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                              APPLICANT: Gong, Joseph K.
APPLICANT: Glomski, Chester A.
TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMIMETIC AGENTS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION
                                                                                                                                      STREET: Clinton
CITY: Rochester
STATE: New York
            CLASSIFICATION:
                      FILING DATE:
                                 APPLICATION NUMBER:
                                                                              COMPUTER:
                                                                                                                          COUNTRY: U.S.A.
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5. 5691157
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Clinton Square,
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                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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97.78;
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                                 US/08/547,197
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RESULT 9
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Best Local S
Matches 118
                                                                                                                                                                                                                                                                         Sequence 1, Application US/08957940 Patent No. 6132981 GENERAL INFORMATION:
COUNIA..

ZIP: 14603

ZOMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: IBM PC compatible

TYPEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                            APPLICANT: Gong, Joseph K.
APPLICANT: Glomski, Chester A.
TITLE OF INVENTION: A METHOD F
TITLE OF INVENTION: EXPOSURE T
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                STATE: N
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                                                                                                                                 STREET: Clinton CITY: Rochester
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                                                                                                                                                                ADDRESSEE:
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118; Conserv
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amino acid
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Y: U.S.A.
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                                                                                                                                                Clinton
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(716) 263-1600
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RESULT 10
US-08-547-197-2
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                                                                                                                      Sequence 2, Application US/08547197 Patent No. 5691157 GENERAL INFORMATION:
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                   APPLICANT: Gong, Joseph K.
APPLICANT: Glomski, Chester A.
TITLE OF INVENTION: A METHOD FY
TITLE OF INVENTION: EXPOSURE TY
                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Rogalskyj, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                           DIESKVDPSKAWGDVKRQISVAAFTVQAAAETLS 439
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Pred. No. 1.2e-34;
9; Mismatches 180
                                                   FOR DETECTING A MAMMAL'S PRIOR TO RADIATION OR RADIOMIMETIC AV
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US-08-957-940-2
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                                                                               Sequence 2, Application US/08957940 Patent No. 6132981 GENERAL INFORMATION:
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Best Local :
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING Patentin Release #1.0, Version #1.
               APPLICANT: Gong, Joseph K.
APPLICANT: GlomsKi, Chester A.
TITLE OF INVENTION: A METHOD FI
TITLE OF INVENTION: EXPOSURE T
   NUMBER OF
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STRANDEDNESS: single
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New York
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   SEQUENCES:
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A METHOD FOR DETECTING A MAMMAL'S PRIOR EXPOSURE TO RADIATION OR RADIOMIMETIC AV
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Pred. No. 1.6e-32;
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Length 760; Indels

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RESULT 12
US-09-079-955-2
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Best Local
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TELEPHONE: (716) 263-1634
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/957,940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Rogalskyj, Peter
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
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OPERATING SYSTEM: PC-DOS/MS-DOS
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14603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTYINLDKAVL 489
                                                                                                      GSH----TLPAL---LENLKLRKQNNGAFNETLFRNQLALATWTIQGAANALS 750
                                                                                                                                                                            ARGDFFRATSRLTTDFGNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGS
                                                                                                                                                                                                             AVKNFTEIASKFSERLQDFDKSNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAP
                                                                                                                                                                                                                                                 AAAEVAGQFVIKLTHDVELNLDYERYNSQLLSFVRDLNG----YRADIKEMGLSLQWLYS
                                                                                                                                                                                                                                                                               TVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEMKTYSLSFDSLFS 326
                                                                                                                                                                                                                                                                                                                        TLDNAAFPFLAYSGIPAVSFCFCED-----TDYPYLGTTMDTYKELIERIPE-LNKVAR
                                                                                                                                                                                                                                                                                                                                                         GSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYETY-ELVEKFYDPMFKYHL 266
                                                                                                                                                                                                                                                                                                                                                                                             GTSNFKVSASPLLYTLIEKTMQNVKHP---VTGQFLYQDSNWASK------VEKL
                                                                                                                                                                                                                                                                                                                                                                                                                               GNYTLRVDCTPLMYSLVYNLTKELKSPDEGFEGKSLYE--SWTKKSPSPEFSGMPRISKL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRSFGTL-KKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERGVAYINADSSIE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGVGTALLLKL 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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Clinton Square, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               760 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.2%; Score 425; DB 3; L
26.5%; Pred. No. 1.6e-32;
Live 93; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/547,197
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GENERAL INFORMATION:

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                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Aspergillus US-09-330-095-1
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APPLICANT: Tony Byun
APPLICANT: Thomas Mathiasen
APPLICANT: Thomas Mathiasen
APPLICANT: Lene V. Kofod
APPLICANT: Mikio Fujii
APPLICANT: Mikio Fujii
APPLICANT: Mikio Fujii
APPLICANT: Mydio Spizuoka
TITLE OF INVENTION: Methods For Producing Protein
TITLE OF INVENTION: Hydrolysates
FILE REFERENCE: 5253 500-US
FULE REFERENCE: 5253 500-US
CURRENT APPLICATION NUMBER: US/09/079,955A
CURRENT APPLICATION NUMBER: US/09/079,955A
CURRENT FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-330-095-1
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                                                                                                                                               Query Match
Best Local
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Patent No. 6127161
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LENGTH: 496
                                                                                                                              Matches
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                     APPLICANT: Kikkoman Corporation
TITLE OF INVENTION: Leucine Aminopeptidase Gene, Recombinant DNA,
TITLE OF INVENTION: Process for Producing Leucine Aminopeptidase
FILE REFERENCE: pH-622
CURRENT APPLICATION NUMBER: US/09/330,095
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: JP164611/1998
EARLIER FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alexander Blinkovsky APPLICANT: Kimberly Brown
                                                                                                                                                                                                                                                        LENGTH: 481
                                                      199
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                                                                                                                              51;
                                                                                                                                               Similarity
                                                                         VKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFG-GIDPQSGAAVVHETVR
VDLWVDSKQENRTTYNVIAQTKGG-DPNNVVALGGHTDSVEAGPGIN-DDGSGIISNLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLRVDCTPLMYSLVYN----LTKELKSPDEGFEGKSLYESWTKKSPSP----EFSGMPRIS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDLWVDSKQENRTTYNVVAQTKGG-DPNNVVALGGHTDSVEAGPGIN-DDGSGIISNLVI 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLGSGNDFEVFFQRLGIASG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKALTQ---YSVKNAVRFLFWTAEEFGLLGSNYYVSHLNATELNKIRLYLNFDMIASPNY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SDYEAFILN-GIPSG
                                                                                                                            Conservative
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25.5%;
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                                                                                                                          Score 131.5; DB 3;
Pred. No. 0.00036;
9; Mismatches 87;
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Pred. No. 0.00024;
9; Mismatches 87
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RESULT 14
US-09-482-273-120
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            TITLE OF INVENTION: AUGUSTIC ACID AND AMINO A TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTI FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-252-991A-18292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: SITE ; LOCATION: (473) ; OTHER INFORMATION: Xaa equals stop translation US-09-482-273-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 120
LENGTH: 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
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                                                                                                                                                                                                                                                         Sequence 18292, Application US/09252991A Patent No. 6551795
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CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
SEQ ID NO 18292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIEE APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
NUMBER OF SEQ ID NOS: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: 71 Human Secreted Proteins FILE REFERENCE: PZ030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENERAL INFORMATION:
APPLICANT: Rosen et al.
                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 32.1 nes 27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     RPKRTLRLVLWTAEEQGGVGAFQY 346
                                                                                                                                                                                                                          Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SDYEAFILN-GIPAG 373
                                                                                                                                                                              Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.3%; score 122.5; DB 4; 32.1%; Pred. No. 0.0027; tive 18; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 473;
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Best Local Similarity
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                                                                                                121 LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
                                                                                                                                 339 VMVGAHLDS-VFEGPGINDNGSGSAAQLE----MAVLLAKA-LPVNKVRFAWWGAEEAGL
   439
                               181 EG-----KSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASG 225
                                                                                                                                                                                                  284 SYEGGIPVIFATYDNGVAWS---QTPDLQLHLVVDVVRKKTETYNVVAETRRG--NPNNV 338
                                                                                                                                                                  64 VILGGHRDSWVFGG---IDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL
                                                                                                                                                                                                                                   10 SWRGSLKV---SYNVGPGFTGNFSTQKVKMH--IHSTNEVTRIYNVIG-TLRGAVEPDRY 63
                                                                                                                                                                                                                                                                        60;
                                                                  VGSTHYVQNLAPEEKKKIKAYLNFDMIGSPNFG------NFIYDGDGSDFGL
QGPPGSAAIERLFEAYFRLR-GQQSEG----TEIDFRSDYAEFFNS-GIAFG 484
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                        5.2%;
25.9%;
                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                        Score 121.5; DB Pred. No. 0.0047;
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                         DB 4;
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Search completed: October 4, 2003, 23:26:47
Job time: 37 secs

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Minimum
Maximum
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No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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 and is derived
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424.5
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length:
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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Gapop 10.0 ,
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2329
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 283308 seqs, 96168682 residues
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Compugen
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ALIGNMENTS

A;Cross-references: GB:M99487; NID:g190663; PIDN:AAA60209.1; A;Experimental source: prostatic carcinoma cell line LMCaPA;Note: sequence extracted from NCBI backbone (NCBIN:121724, C;Superfamily: transferrin receptor C;Keywords: surface antigen; transmembrane protein RESULT A56881 Qy C;Accession: A56881
R;Israeli, R.S.; Powell, C.T.; Fair, W.R.; Heston, W.D.
Cancer Res. 53, 227-230, 1993
A;Title: Molecular cloning of a complementary DNA encoding A;Reference number: A56881; MUID:93113576; PMID:8417812
A;Accession: A56881 prostate-specific membrane antigen - hu
C; Species: Homo sapiens (man)
C; Date: 03-Nov-1995 #sequence_revision В Qy 밁 Qy 밁 δÃ 밁 밁 Q 뫄 Qy A; Molecule type: mRNA A; Residues: 1-750 <ISR> A; Status: preliminary Matches Query Match Best Local : 361 609 301 549 241 489 181 429 121 LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLIKELKSPDEGF 180 369 309 tch 98.2%; al Similarity 98.0%; 433; Conservative 61 L YPLYHSYYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYA EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSG DRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL DRYVILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGL YPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYA EGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSG LGSTEWAEENSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGF 6, Score 2288; DB 2; Pred. No. 1.8e-163; 6; Mismatches 3; human 03-Nov-1995 #text_change Length Indels ជ PID:g190664 NCBIP: 121725) prostate-specific membra 17-Mar-2000 0 Gaps 360 300 120 899 548 240 488 428 368

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C;Species: Arabido
C;Date: 20-Apr-200
C;Accession: T4765
R;Obermaier, B.;
submitted to the F
A;Reference number
                                             RESULT 3
747631
Peptidase-like protein - Arabidopsis thaliana
Piptidase-like protein T5N23.80
N;Alternate names: protein T5N23.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
T30154
hypothetical protein R57.1 - Caenorhabditis elegans
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A; Introns: 40/1: 145/1; 230/1; 275/3; 313/1; 344/2; 405/1; 453/2; 576/2; 671/2; 713/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U88179; PIDN:AAB52660.1; GSPDB:GN00028; A;Experimental source: strain Bristol N2; clone R57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
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A; Residues: 1-751 <FAV>
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                                                                                                                                                                                                                                                                                                                                KTYLPQLKTTISGINVSRSDFEDIRTQYAL----LSKSAQDLLTMSKKFQETIHFTQHSF
                                                                                                                                                                                                                                                                                                                                                               RKYADKI-----YNISMKHPQEMKT-YSLSFDSLFSAVKNFTEIASKFSERL----QDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGRKTLYDTWMKVFPDKK-AGVPKIRVPGGGSDHAPFLNFAGVPV--INFTFKNYTT--W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPD--EGF
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               Protein
                                   Ottenwaelder, B.;
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                Sequence
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Pred. No. 2.8e-39;
                  Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from GB/EMBL/DDBJ
                                 Duchemin, D.; Zeitler, K.; Mewes, H.W.; Lemcke,
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T19751
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-703 < OBE>
A;Cross-references: EMBL:AL138650
A;Experimental source: cultivar Columbia;
                                                                                                                                                                                                                                                 submitted to the EMBL Data A; Reference number: Z19173 A; Accession: T19751
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A;Introns: 326/3; 407/3;
A;Note: T5N23.80
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A; Map position: X
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Best Local Similarity
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                                 Query Match
Best Local Similarity
Matches 147; Conserv
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     MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNE-
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                                               23.4%;
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                                     84;
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Mesidues: 1-1483 <WIL>
A; Cross-references: EMBL: Z78417; PIDN: CAB01688.1;
A; Cross-references: clone C35C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C35C5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                               A; Introns: 61/1; 203/3; 248/1; 293/3; 331/1; 437/1; 485/2; 523/2; 556/1; 595/3; 620/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILLRMNNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESK 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GMIGSTEWIEENVLNLGASAVAYLNVDCAVQGS-GFFAGATPQLDGLLVDVLK--LDPDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt AKRRELNDRLMLVERGFLDAEGIKGKEWFKHLVYGPAAEPESKLGFFPGIADAIAMNASE}
                                                                                                                                                                                                                                                                                                                                                                                  Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 579; DB 2;
Pred. No. 2.2e-35;
                                               Score 545.5;
Pred. No. 2.1e-32;
4; Mismatches 181;
                                                                                                                                                                                                                                                                                                          from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          698
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                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162;
                                                                                                                                                                                                                                GSPDB:GN00028; CESP:C35C5
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                                            Length 1483;
  Indels
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  61;
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transferrin receptor - rat (fragment)
(;Species: Rattus norvegicus (Norway rat)
(;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Aug-1999
(;Accession: A34549
R;Roberts, K.P.; Griswold, M.D.
Mol. Endocrinol. 4, 531-542, 1990
A;Reference number: A34549; MUID:91125359; PMID:2126342
A;Reference number: A34549; MUID:91125359; PMID:2126342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-622 < ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A34549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: transferrin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor; transmembrane protein
                                                                                                                                                                                                                                                  MGGSAPP----DSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDVKRQISVAAFTVQAA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEM-KTYSL--SFDSLFSAVK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKIQNIMGYIKGSQEPDKFVLVSNHYDAWTYGAVDPNSGTSTLLEVSRALKQYQNQTGWI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKE-GWR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P---IDGKYLYRNSNWISK----
                                                                                                                                                                 GDYGAVGPTEWLEGYLSSLHLKAFTYINLDKVVLGTSNFKVSASPLLYTLMGKIMQDVKH
                                                                                                                                                                                                                                                                                           AVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFG-TLKKEGWRPRRTILFASWDA 115
                                                                                                                                                                                                                                                                                                                                     MEGNCPPSWNIDSSCK--LELSQN------QNVKLTVNNVLKETRILNIFGVIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QFKLLQKTVLELSEIVQRRNVSKLEELPFGSRVDINNRLIEFEKCFINPHGAIGNPQARH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLFHPSPDNWYDGDAISQVHDLISKISNSTD-SKELGKLSRQLAKEIALVNVA 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGI-----ASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLVYNLTKELKSPD--EGFEG-KSLYESWTKKSPSPEFSGMPRISKL-GSGNDFEVFFQR 219
                                     ETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYA 293
                                                                                                                        PDEGFEGKSLY--ESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNW 233
                                                                                                                                                                                                        EEFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFTEIASKFSERLQDFDKSN------PILLRM-MNDQLMFLERAFIDPLGLPDRPFYRH 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IECILKFTESKILPYDLNEL-----MDDSIFEYLPKLEDRLNKTLMIGTKTDYLLDAQK 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGIPIVFFITSSLDAPPT------YPLYHTIYETPYLIENIMDPGYKVHKAIAGMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVLRSAAANVEQPNPTEMEQGRKTLYDSWKYYAPSKNNRSTHPYQRIPAGGSDHLPFFDY 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARSILFAHWDAEEYGLIGSTEFAEEYRLQLMRRAVAVINMD-LIGGNQTLLGLSNPTVA 494
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
EDYPYLGTKLDTYEILIQKVPQLNQMVRTAAEVAGQFIIKLTHDIELTLDYEMYN
                                                                                                                                                                                                                                                                                                                                                                                                                                       19.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 445.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                IEELSLDNAAFPFLAYSGIPAVSFCFCED-
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A;Description: meusacce con-
C;Superfamily: transferrin receptor
C;Keywords: glycoprotein; iron transport; receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA A;Rosidues: 'AL',27-149,'Q',151-301 <RES> A;Residues: 'AL',27-149,'Q',151-301 <RES> A;Cross-references: GB:M29618; NID:g193272; PIDN:AAA37616.1; A;Cross-references: GB:M29618; NID:g193272; PIDN:AAA37616.1; A;Cross-references: GB:M29618; NID:g193272; PIDN:AAA37616.1; A;Cross-references: Garage and Serve as an internal signal sequence. C;Comment: The expression of this receptor, involved in the r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 7-19;158-175,'X',177-179;'DESL','AY',189,'IEN',193,'FXEF',195;196,197-208
A;Residues: 7-19;158-175,'X',177-179;'DESL','AY',189,'IEN',193,'FXEF',195;196,197-208
A;Rote: these tryptic fragments have been ordered by homology with the human sequence
R;Stearne, P.A.; Pietersz, G.A.; Goding, J.W.
J.Immunol. 134, 3474-3479, 1985
A;Title: cDNA cloning of the murine transferrin receptor: Sequence of trans-membrane
A;Reference number: 149662; MUID:85159078; PMID:2984291
A;Accession: 149662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: S29548; A26735; D24550; I49662
C;Accession: S29548; A26735; Daningo, D.L.; Thomas, M.L.; Chain, A. submitted to the EMBL Data Library, January 1991
A;Reference number: S29548
                                                                                                             F;58-61/Region: stop-transfer sequence F;62-99/Domain: transmembrane #status predicted <TMS>F;62-99/Domain: transmembrane #status predicted <EXT>F;89-763/Domain: extracellular #status predicted <EXT>F;101-763/Product: 85K serum transferrin receptor #status predicted <MAT>F;253,319,730/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Grego, B; Van Driel, I.R.; Stearne, P.A.; Goding, J.W.;
Eur. J. Biochem. 148, 485-491, 1985
A;Reference number: A24550; MUID:85203852; PMID:2986964
A;Accession: D24550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Endocytosis of the transferrin receptor requires A;Reference number: A26735; MUID:87187639; PMID:3568132 A;Accession: A26735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 1-82 < ROT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: S29548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                              A; Description: mediates cell iron uptake by binding, internalizing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X57349; NID:g54914; PIDN:CAA40624.1; PID:g54915 R;Rothenberger, S.; Iacopetta, B.J.; Kuhn, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-763 <TRO>
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                               Query Match
Best Local
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                               Similarity
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26.7%;
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Score 435; DB 1; I
Pred. No. 1.5e-24;
88; Mismatches 171;
                                                                                                                                                                                                                                                                          <INT>
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                                                           Length 763;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PID:g193273
r of similar or
e cytoplasm and
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   78;
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   Gaps
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1 MGGSAPP----DSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRG

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J. Biol. Chem. 265, 19077-19081, 1990
A; Title: Serum transferrin receptor is a truncated form of A; Reference number: A36597; MUID:91035436; PMID:2229063 A; Molecule +----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:X01060; NID:g37432; PIDN:CAA25527.1; PID:g37-R; McClelland, A.; Kuhn, L.C.; Ruddle, F.H.
Cell 39, 267-274, 1984
A;Title: The human transferrin receptor gene: genomic organization, A;Reference number: A90856; MUID:85048936; PMID:6094009
A;Accession: A90856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: CD71; p90
N;Contains: 85K serum transferrin receptor
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 22-Jun-1999
C;Accession: A93343; A90856; A36597; S54327; S09039; A03259
R;Schneider, C; Owen, M.J.; Banville, D.; Williams, J.G.
Nature 311, 675-678, 1984
    R; Alvarez,
Biochem. J.
                                                                                                             A; Experimental source: serum R; Coppolino, M.; Migliorini, M.; Argraves, W.S.; Dedhar, Biochem. J. 306, 129-134, 1995
A; Title: Identification of a novel form of the alpha(3): A; Reference number: S54327; MUID:95169043; PMID:7864799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Primary structure of human transferrin receptor deduced A;Reference number: A93343; MUID:85012743; PMID:6090955 A;Accession: A93343
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                                      A; Molecule type: protein
A; Residues: 288-302; 694-708; 721-730 <COP>
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                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 101-103,'x',105-108,'x',110-119 <SHI>
                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M11507; NID:g339515; PIDN:AAA61153.1; PID:g339516
R;Shih, Y.J.; Baynes, R.D.; Hudson, B.G.; Flowers, C.H.; Skikne, B.S.; Co
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-760 < MCC>
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A; Residues: 1-760 <SCH>
                                                                                              A; Accession: S54327
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    , E.; G
J. 267,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 YAVVLRKYADKIYNISMKHPQEMKT----YSLSFDSLFSAVKNFTEIASKFSERLQDFDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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; Girones,
67, 31-35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHN------KYAGESFPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYDALFDIESKVDPSKAWGDVKRQISVAAFTVQAAAETLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSPDEGFEGKSLY--ESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTK
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    N.;
                          Davis,
                          R.J.
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                                                                                                                                                                                                                                                                                                                                                                               J.D.
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A;Description: mediates cell iron uptake by binding, intern C;Superfamily: transferrin receptor C;Keywords: glycoprotein; iron transport; receptor; transme F;1-57/Domain: intracellular #status predicted <INT> F;20-24/Region: tyrosine-based endosomal/lysosomal sorting F;58-61/Region: stop-transfer sequence F;62-89/Domain: transmembrane #status predicted <TMS> F;62-89/Domain: transmembrane #status predicted <TMS>
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A;Residues: 1-19,'C',21-61 <ALV>
A;Residues: 1-19,'C',21-61 <ALV>
A;Rote: mutant defective in endocytosis
A;Note: mutant defective in endocytosis
C;Comment: This transmembrane glycoprotein exists as a dimer of similar or
C;Comment: The amino end of each chain lies within the cytoplasm and
embrane, may also serve as an internal signal sequence.
C;Comment: The expression of this receptor, involved in the regulation of c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;89-760/Domain: extracellular *status predicted <EXT> F;101-760/Product: 85K serum transferrin receptor *status F;251,317,727/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Comment:
C; Genetics:
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C; Function:
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A;Cross-references: GDB:120433; OMIM:190010
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Best Local :
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                                                                                                           645 ARGDFFRATSRLTTDFGNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGS
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                                                                                                                                                                                                                                                                                                                                   536 TLDNAAFPFLAYSGIPAVSFCFCED-----TDYPYLGTTMDTYKELIERIPE-LNKVAR 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 GNYTLRVDCTPLMYSLVYNLTKELKSPDEGFEGKSLYE--SWTKKSPSPEFSGMPRISKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 VRSFGTL-KKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERGVAYINADSSIE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 TQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHET 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110;
                                                    SSHNKYAGESFPGIYDALFDIESKVDPSKAWGDV--KRQISVAAFTVQAAAETLS 439
                                                                                                                                                                                                                                                                         TVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEMKTYSLSFDSLFS
                                                                                                                                                                                                                                                                                                                                                                                        GSGNDFEVFFORLGIASGRARYTKNWETNKFSGYPLYHSVYETY-ELVEKFYDPMFKYHL
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GSH-----TLPAL----LENLKLRKQNNGAFNETLFRNQLALATWTIQGAANALS
                                                                                                                                                          AVKNFTEIASKFSERLQDFDKSNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAP
                                                                                                                                                                                                                    AAAEVAGQFVIKLTHDVELNLDYERYNSQLLSFVRDL----NQYRADIKEMGLSLQWLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTYINLDKAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mediates cell iron uptake by binding, internalizing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
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Pred. No. 7.2e-24;
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C;Accession: A48592
R;COllawn, J.F.; Lai, A.; Domingo, D.; Fitch, M.; Hatton, J. Biol. Chem. 268, 21686-21692, 1993
A;Title: YTRF is the conserved internalization signal of A;Reference number: A48592; MUID:94012749; PMID:8408022
A;Accession: A48592
A;Status: preliminary
A;Molecule type: mRNA

transferrin receptor protein - Chinese C;Species: Cricetulus griseus (Chinese C;Date: 03-May-1994 #sequence_revision

hamster) 03-May-1994

#text_change

20-Aug-1999

, s.;

transferrin receptor,

an

I.S.

A48592

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C:Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; transm F;19-22/Region: coated pit mediated internalization signal F;70-88/Domain: transmembrane #status predicted <TRM>F;23/Binding site: phosphate (Ser) (covalent) #status predicted F;70/Binding site: palmitate (Cys) (covalent) #status predicted F;70/Binding site: palmitate (Cys) (covalent) #status predicted F;261,326,391,738/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                         Ş
                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:x55348
A;Note: 581-His and 736-Gln were also found as the result of C;Comment: This protein mediates the endocytosis of the iron
                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Gallus gallus (Chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JM0570; S16855
R;Gerhardt, E.M.; Chan, L.N.L.; Jing, S.; Qi, M.; Trowbridge, I.S.
Gene 102, 249-254, 1991
A;Title: The cDNA sequence and primary structure of the chicken transferrin receptor.
A;Reference number: JH0570; MUID:91340160; PMID:1874449
A;Accession: JH0570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
JH0570
                                                                                                                                                                                                                                                                                         C; Superfamily: transferrin receptor
                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-776 <GER>
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A;Cross·references: GB:119142; NID:g304528; PIDN:AAA03576.1; PID:g304529 C;Superfamily: transferrin receptor C;Keywords: endocytosis; glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transferrin receptor - chicken
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                                                                                                                 Similarity
                                           WRG----SLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILG
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              WKGAIHSCKVT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEKTNRFVVREINNRIMKVEYHFLSPYVSPRESPFRHIFWGSGSHTLTA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCRDYAVVLRKYADKIYNISMKHPQ----EMKTYSLSFDSLFSAVKNFTEIASKFSERLQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRYIVVGAQRDAWGPGAAKSSVGTGLLLKLAQAFSDMVSRGGFKPSRSIIFASWSAGDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRYVILGGHRDSWYFGGIDPQSGAAVVHETVRSFGTL-KKEGWRPRRTILFASWDAEEFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGGSAPPDSSWRGSLKVSYNVGPGFTGNESTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENLKLRQKNSSAFNETLFRNQLALATWTIQGVANALS 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDIESKVDPSKAWGDV--KRQISVAAFTVQAAAETLS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDKSNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METNCPP--SWNTDSLCKLESSQGINVNLS-----VNNVLKETRILNIFGVIKGFEEP
                                                                                            Conservative
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                                                                                                            17.8%;
27.1%;
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24.9%; Pred. No. 9.3e-24;
tive 88; Mismatches 182
          ---TKHESQIMVKLDVNNSMKDRKILNIFGAIQGFEEPDRYVVIG
                                                                                            84;
                                                                                      Score 413.5; DB 1;
Pred. No. 6.5e-23;
4; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. >...
8; Mismatches
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                                                                                      Gaps
                                                 67
          419
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C; Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-811 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S56848
A; Accession: S57149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YJR126c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J2050
C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 19-A
C;Accession: S57149
R;Rose, M.; Koetter, P.; Entian, K.D.
Submitted to the Protein Sequence Database, September 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: MIPS:YJR126c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: Z49626;
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                                       VYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIY--
                                                                                                                   WTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYH--S 246
                                                                                                                                                        AHAAILRRRALVYLNLDNAISGT-NFHCKANPLLQDVIYEAAK--LTEFNGHEDWSLFDH 562
                                                                                                                                                                                                                                                                                                                FQIGPGSNIKDFGSFTGPSSSIDKVHLHNELTYNIKEMSSVEVSIPG-IFTEGEIIIGAH 445
                                                                                                                                                                                  DNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGFEGKSLYES 188
                                                                                                                                                                                                                                                                       RDSWVFGGI-DPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAE 128
VFDSPTWLEKFTNSDYKLHNTMAMFVGLTTLMLSENELARFN-----THVYLKKIYNW
                                                                                                                                                                                                                                      RDSLASSSAGDANSGSAILLEIARGMSKLLKHGWKPLRPIKLISWDGERSGLLGSTDYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPSKAWGDVKRQISVAAFTVQAAAETL 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEELLAYQEEF----LPYIKEVRELGLTLDWLFFARGDFQRAVTALRRDIANSDGENRVI 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVVLRKYADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQRDSWGPGVAKAGTGTAILLELARVISDIVKNEGYKPRRSIIFASWSAGDYGAVGATEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHRDSWVFGGIDPQSGAAVVHETVRSFGTL-KKEGWRPRRTILFASWDAEEFGLLGSTEW 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NKDEEYRFLDTKGDTLENLRKI-DNLDALLAAAAEVAGQAALRLTHDHELFLDIGRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEGYSAMLHAKAFTYISLDAPVLGASHVKISASPLLYMLLGSIMKGVKNP--AAVSESLY
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD:S0003887
                                                                            -KYTSNATISLLDGLSSYTSFQYHLGVPAAHFQF----NANDTSG-AVYHSNS
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27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID:g1015854;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 399; DB 2;
Pred. No. 8.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:g1015855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                              72;
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RESULT 11
T40289
hypothetical protein SPBC354.09c - fission yeast (Schizosaccharomyces pombe)
hypothetical protein SPBC354.09c - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-mar-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T40289
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C; Superfamily: s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-794 <WOO>
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A;Experimental source: strain 972h-; cosmid c354
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probable peptidase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: E85075
                                                                     RESULT 12
E85075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Local Similarity 25.0%;
Les 105; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTGS-KIS---SPGLEVNV------LQDIEDKQKIINIMAQIDG-YESDQILVVGAPR 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILGGHR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLYYNLTKELKSPDEGFEGKSLYESW 189
                                                                                                                                                                                                                                                                                                                                                DYTS-----TPMPFLGSCED
                                                                                                                                                                                                                                                                                                                                                                              TKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYE 249
                                                                                                                                                                                                                                                                                                                                                                                                                WKESLEAKAVAYINVDVAVSGD-TFTARTVPGLKKVIQRAFDVANEEDEMKAANIITDDF
                                                                                                                                                                                                                                        HPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFD----KSNPILLRMMNDQLMFLF
                                                                                                                                                                                                                                                                                                            TYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMK 309
                                                                                                                                                                                                                                                                            TVSWIDTFGSEYWENAARLGKIWSYLILFLANDPVVPYDLEDEINGVGEMLKRIPEIPGA 667
                                                                                                                                                                                                        NALDLRKINEEFSELLESLIRFEDEIREWKSLMMHNSYTVSVKKHP-ELEGYNAKLARFE 726
                                                                                                                                        RSFLDEAGLPGHEWYKHLIYGPNLRNSHS-QLFPSIFDALLYGDVEA-----AQKEVKR
                                                                                                                                                                     RAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALF--DIESKVDPSKAWGDVKR 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 355; DB 2; 1
Pred. No. 1.6e-18;
10; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSPDB:GN00067; SPDB:SPBC354.09c
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S67153
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R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Col. Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: E85075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <STO>
A;Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YOR256c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O5330
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: AT4g07670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain $288C C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-809 <JAU>
A; Residues: 1-809 <JAU>
A; Cross-references: EMBL: 275164; NID: g1420578; PIDN: CAA99478.1;
A; Cross-references: EMBL: 275164; NID: g1420578; PIDN: CAA99478.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S67143
A; Accession: S67153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: S67153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: secretory protein SP134
C;Keywords: transmembrane protein
F;126-142/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 15R
C;Superfamily: secretory protein SSP134
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: MIPS:YOR256c
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                                                                                                                                                                                                                                                                  RTILFASWDAEEFGLLGSTEWAEDNSRLLQER------GVAYINADSSIEGNYTLR 155
                                                                                                                                                                                                                                                                                                           IPNIVGKIEGREQSDKAIIIAASRNSINFGTTYPNFGTAALLSIVQLFQEVKYKFGWKPL
                                                                                                                                                                                                                                                                                                                                              IYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLK-KEGWRPR 105
                              YHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEMKTYSLSFDS
                                                                                                                                                 IETHPLLKKF-FNRNAH-GNFDISVDNVQHYGDWT----PFLANGIP-VSVISSD----
                                                                                                                                                                                        VDCTPLMYSLVYNLTKELKSPDEGFEGKSLYESWTKKSPSPEF-SGMPRISKLGSGNDFE 214
                                                                                                          VFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDP------
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ELIDDPLLHFDIISY --
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                                                                                                                                                                                                                                                                                                                                                                                               78; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database,
                                                                                                                                                                                                                                                                                                                                                                                                               Score 240.5; DB 2
Pred. No. 6.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GTLKKEGWRPRRTILFASWDAEEFGLLGS
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-VEDIDERLORLEOAYPEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                             -DKFERVEKILEDEQNQQSVKDLLVYL 629
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C:Reywords: glycoprotein C:Reywords: glycoprotein 7.7%; Score 179.5; DB 2; Length 783; Best Local Similarity 19.7%; Pred. No. 2.3e-05; Best Local Similarity 19.7%; Pred. No. 2.3e-05; Matches 93; Conservative 82; Mismatches 169; Indels 127; Gaps Qy 15 LKVSYNVGPGFFGNESTOKVKMHIHST-NEVTRIYNVIGTLRGAVEPDRYVILGGHRDSW Qy 16
Keywords: 91 139,213/Bind 139,213/Bind Query Match Best Local S Matches 93 431 431 133 491 186 543
Keywords: 91 139,213/Bind 139,213/Bind Query Match Best Local S Matches 93 Matches 93 431 133 133 491 186
Keywords: 91 139,213/Bind 139,213/Bind Query Match Best Local S Matches 93 Matches 93 431 431 133
Keywords: 91 139,213/Bind 139,213/Bind Query Match Best Local S Matches 93 Matches 974 74
Keywords: gl 139,213/Bind 139,213/Bind Query Match Best Local s Matches 93 Matches 15
A;Gene: SSP134 A;Cross-references: SGD:S000609 A;Map position: 16L C;Superfamily: secretory protei
Molecule type: Residues: 66-14 Note: the author Note: the author Genetics:
Title: Selection Reference number Accession: JH048
A; Restaues: 1.783 <ben> A; Cross-references: EMBL:Z73532; NID:g1370370; A; Experimental source: strain S288C (AB972) A; Experimental source: Strain S288C (AB972) A; Experimental source: Strain S288C (AB972) Cone 107 111-118 1001</ben>
A; Reference number: (A; Accession: S65188 A; Molecule type: DNA A; Doctor 1-783 (7)
R; Benes, V.; Rechmann, S.; Nentwick submitted to the Protein Sequence
C; Species: Saccharomyces cerevisiae C; Date: 10-Dec-1994 #sequence_revision C: Accession: S65188. JH0485
RESULT 14 S65188 secretory protein SSP134 - N; Alternate names: protein
Db 785 IDLIGKVLHQSAALFVE
Qy 424 ISVAAFTVQAAAETLSE
Db 733 GLPNRSFYKNVLFGPTLIQEDKSKNGGNVDFWTFPGVMDAIYDDD-
373 1
324
FSAVKNFTEIASKFS :: ::: ::: ::: :::

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A:Cross-references: GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF83630.1; GSPDB:GN A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.C.R.; Canestics: annotation C.Cenestics: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C;Accession: G82759
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C;Superfamily: Xylella fastidiosa hypothetical protein XF0820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein XF0820 [imported] - Xylella fastidiosa (strain 9a5c) C; Species: Xylella fastidiosa
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A; Residues: 1-529 <SIM>
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A; Status: preliminary
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439
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                                                                                                                                                                                                                                                                                                                                                                                                     270 SEVITSHNVAARLQGCAHPDETVIYSAHWDHLGVGAPDAKGDTIFNGALDNASGTAALLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               669
                                                                  196 PEFSGMPRISKLGSGNDFEVFFQRLGIASGRA 227
                                                                                                                                     385 QGPTRDFGIYGTAKLDLLDMLKQVAAGWKLRYTLD---PTPEAGHFFRSDHFSFAKR---
                                                                                                                                                                                                    146 ---SSIEGNY-TLRVDCTPLM-----YSLVYNLTKELKSPDEGFEGKSLYESWTKKSPS 195
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                                                                                                                                                                                                                                                                                                          90 TVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERGVAYINAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 NEVTRIYNVIGTLRGAVEPDRYVILGGHRD------SWVF-GGIDPQSGAAVVHE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
66; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.4%; Score 173; DB 2; Length 529; llarity 31.1%; Pred. No. 4e-05; Conservative 30; Mismatches 70; Indels
-GIPAIS-YSAGQDMEVG----GVAAGKA 461
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Search completed: October 4, Job time: 41 secs

2003, 23:26:01

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Title:
Perfect score:
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Listing first 45 summaries
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 2329
2097.5
571.5
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158
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_bage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_virus:*
13: sp_virus:*
14: sp_unclass
15: sp_bacteri
17: sp_archeap
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Match
  100.0
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1 MGGSAPPDSSWRGSLKVSYN......QISVAAFTVQAAAETLSEVA 442
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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sp_vertebrate:*
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  614
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4 Q9HBA9

4 Q8TAY3

16 Q8PGX5

5 Q93332

6 Q8HZV3

10 Q94JV4

10 Q94JV4

11 Q94JH2

11 Q94JH2

3 Q08693

11 Q8C872

3 Q08693

11 Q9PF58

16 Q9PF58

16 Q9PF58

16 Q8P530
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           Q9hba9 homo sapien Q8tay3 homo sapien Q8tay3 homo sapien Q8tay3 homo sapien Q94j332 caenorhabdi Q94jh4 oryza sativ Q8lq6l oryza sativ Q8lq6l oryza sativ Q94jh3 oryza sativ Q94jh3 oryza sativ Q94jh3 arabidopsis Q86693 saccharomyc Q8c872 mus musculu Q08919 saccharomyc Q9pf58 xylella fas Q8p530 xanthomonas Q9p538 caulobacter
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 Q8pps0 xanthomonas
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45	44	43	42	41	40	39	3 8	37	36	ω 5	34	33	32	31	30	29	28	27	26	25		23	22		20	19	18	17
117	120	120	120.5	121	121.5	122.5	122.5	122.5	126	126.5	128.5	130.5	131	131	133	133.5	136	137.5	138	139.5	142.5	144.5	146.5	146.5	148	149	151	152.5
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Q8VUS4	Q8PEF6	Q8EF07	Q9F2X2	Q8PRD7	д9нzд8	Q9Y5X6	Q9Y646	Q8NBZ1	Q53737	076552	Q8EDI3	P96264	Q9Z1Y1	Q9JLV0	Q04033	Q8PFH7	Q9WVJ3	Q8TY04	Q8CK35	082996	08ьне8	Q93EJ5	Q8P3Z6	Q8P625	Q9KLD3	P96152	Q8EBH7	Q9A3U5
മ			Q9f2x2 streptomyce	Q8prd7 xanthomonas	8 pse	homo			Q53737 streptomyce	а		P96264 mycobacteri	Q9zlyl rattus norv	0	Q04033 saccharomyc	Q8pfh7 xanthomonas			Q8ck35 streptomyce	082996 aeromonas p	Q8phe8 xanthomonas	Q93ej5 bacillus li	Q8p3z6 xanthomonas		ω	P96152 vibrio chol	Q8ebh7 shewanella	Q9a3u5 caulobacter

ALIGNMENTS

О Ве ма	RESULT OOHBAO OO O
Query Match 100.0%; Score 2329; DB 4; Length 442; Best Local Similarity 100.0%; Pred. No. 1.6e-170; Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	O9HBA9 O9HBA9 O9HBA9; PRELIMINARY; PRT; 442 AA. O9HBA9; O1-MAR-2001 (TrEMBLrel. 16, Created) O1-MAR-2001 (TrEMBLrel. 23, Last annotation update) O1-MAR-2001 (TrEMBLrel. 23, Last annotation update) O1-MAR-2001 (TrEMBLrel. 23, Last annotation update) Prostate-specific membrane antigen-like protein. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606; [1] TISSUB=Liver; O'Keefe D.S., Bacich D.J., Heston W.D.W.; "Expression Profile of Prostate-Specific Membrane Antigen (PSMA) versus a Prostate-Specific Membrane Antigen-Like Gene in Normal Tissues, Prostate-Specific Membrane Tissues, Prosta

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2002) to the ENERL; BC025672; AAH25672.1; -
Interpro; IPR003137; PA.
Pfam; PF02225; PA; 1
Pfam; PF04253; TFR_dimer; 1.
PROSITE; PS50840; PA; 1.
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01-JUN-2002
01-MAR-2003
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                  Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBTAY3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8TAY3
                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                          1 MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to folate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRQISVAAFTVQAAAETLSEVA 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMNDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL
LGSTEWAEENSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGF
                                                                                 DRYVILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGL
                                                                                                                                                                      MGGSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydrolase
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Primates;
                                                                                                                                                                                                                                                                                                                                            80597 MW;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Prostate-specific memb
                                                                                                                                                                                                                                                                       Score
Pred.
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                                                                                                                                                                                                                                                                                                                                            AF79A10CA2BF9DF4 CRC64;
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RESULT Q8PGK5
ID Q8
AC Q8PGK5
ID Q8
AC C8

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XX MEDLINE-22022145; PubMed-12024217;

XX da Silva A.C.R., Ferro J.A., Reinach F.C., Eamargo L.E.A.,

XX Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

XX Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

XX Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

XX Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

XX Cicarelli R.M.B., Coutlinho L.L., Cursino-Santos J.R., El-Dorry H.,

XX Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

XX Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.M. V.F.,

XX Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

XX Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

XX Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

XX Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

XX Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

XX Piniola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

XX Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

XX Setubal J.C., Kitajima J.P.;

**Gromparicon of the Corocco of the Variation of the Corocco of the Coroc
                                                                                                                                                                                                                                                           Query Ma
Best Loc
Matches
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01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 417:459-463(2002).
EMBL; AE012011; AAM38454.1;
Pfam; PF04253; TFR_dimer; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xanthomonadaceae;
NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8PGK5
                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Comparison of the genomes of two Xanthomonas pathogens host specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XAC3611
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                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                 Н
                                                                                                                                                                                                                                                                                                 Similarity
YPDQWVVRGNHRDGWVFGAADPLSGTTALLAEAKAIGELAKQGQRPKRTLVYASWDGEEA
                                                       EPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEF
                                                                                                                               LGGPVAPE-DWRGALPITYRIG-----GDAKARVHLKVDADWGSQTIYNVIATLRGSE
                                                                                                                                                                                             MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNE--VTRIYNVIGTLRGAV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRQISVAAFTVQAAAETLSEVA 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRQIYVAAFTVQAAAETLSEVA 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKIYSISMKHPQEMKTYSVSFDSLFSAVKNFTEIASKFSERLQDFDKS-------
                                                                                                                                                                                                                                                                                                                                                                                                  614 AA;
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                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                              66255 MW;
                                                                                                                                                                                                                                                                                              24.5%;
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22,
23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                           Score 571.5; DB 16;
Pred. No. 2.3e-35;
8; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                  636C3FE15BF008DD CRC64;
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                                                                                    Query Match
Best Local (
                                                                                                                        MEROPS; M28.011;

WormPep; C35C5.2; CE08584.

InterPro; IPRO03137; PA.

Pfam; PF02225; PA; 2.

Pfam; PF04253; TFR_dimer; 2.

PROSITE; PS50840; PA; 2.
                                                                                                                  PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                               01-FEB-1997 (TREMBLIEL 02,
01-FEB-1997 (TREMBLIEL 02,
01-MAR-2003 (TREMBLIEL 23,
                                                                                                                                                                                  "Genome sequence of the nematode C.elegans: investigating blology."; Science 282:2012-2018(1998).
EMBL; Z78417; CAB01688.1;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                               093332;
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                                                                                                                                                                                                                                                                Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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                                                                           al Similarity
147; Conserv
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                  45
                                                                                                                  PS50840; P.
1483 AA;
RKIQNIMGYIKGSQEPDKFVLVSNHYDAWTYGAVDPNSGTSTLLEVSRALKQYQNQTGWI
           TRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLKKE-GWR
                                     MKGDA-VNADFQGKLNVTYRYGPGLINN----QKLRVTVHAENEERSVIVVELISRLRLNF
                                                     MGGSAPPDSSWRGSLKVSYNVGPGFTGNFSTQKVKMHIHSTNE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDVKRQISVAAFT
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                                                                           Conservative
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                                                                                    23.4%;
31.1%;
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168164 MW;
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                                                                          Score 545.5; DB 5;
Pred. No. 8.5e-33;
4; Mismatches 181;
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                                                                                                                  AE07537AD85E8FFC CRC64;
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Query Match
Best Local Sin
Matches 112;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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01-MAR-2003
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                       TWRTDFPCKLVSSP-----SKNVKLTVNNVLKEIKILNIFGVIKGFEEPDRYVIVGAQ 416
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                                    KF-----SGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRD 291
                                                                                                                                                                                                                                                                                                          RDSWVFGGIDPQSGAAVVHETVRSFGTLKKEG-WRPRRTILFASWDAEEFGLLGSTEWAE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGDVKRQISVAAFTVQAA
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                                                                                                                                     ESWTKK-----SPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETN 236
                                                                                                                                                                                                                               DNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGFEGKSLY--
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-FCFCEDTDYPYLGTTMDTYDVLSKRVPQLNRMARAAAEVAGHLVIKLTIDFELNLN---
                                                                                                                                                                                   GYLSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYSLIEKMMQDVKNP---VTGQSLYRD
                                                                                                                                                                                                                                                                                RDAWGPGAAKSSVGTSLLLNLAQILSDMVIKGQFKPSRSIVFASWSAGDFGAIGATEWLE
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24.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 415.5; DB 6;
Pred. No. 3.1e-23;
0; Mismatches 169;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02325; PA; 1.
Pfam; PF04253; TFR_dimer; 1.
PROSITE; PS50840; PA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; AP002972; BAB55507.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P063BD12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptidase-like protein. P0638D12.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gramene; Q94JH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q94JH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003137; PA.
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     521
                                                           347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WDAEEFGLLGSTEWAEDNSRLLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKE 172
SSNQLKKDSMKIRSLNDRLMQAERAFTNREGLFKREWFKHLVYGPSEQNDWESASYPGVE
                                                                                                                                                          RDYAVVLRKYADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFD---
                                                                                                                                                                                                                        SCGWRNSEIQG----
                                                                                                                                                                                                                                                                                                                              VQDPDN--SSQAVYDSWVKSNISPLDQAIPYI-----
                                                                                                                                                                                                                                                                                                                                                                                LKSPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTK- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                              WDAEEYGL ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGDAAP-ADWQGREGSPYYRLGPGPAILNLTYTGN-------DTMATIENVFA 354
                                                  ----KSNPILLRMMNDQLMFLERAFIDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIY 401
                                                                                                        --SVGTLQAYTKVVEN-----EVRGTAISCSPLHNAIRALKTAATKVNGERKELQRQL
                                                                                                                                                                                                                                                                        -- NWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESKVDPSKAWGD--VKRQISVAAFTVQAAAETLS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKFVMREINDRIMKVEYHFLSPYVSPRESPFRHIFWGSGSHT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               621 AA;
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19,
23,
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yta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Mismatches 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 412; DB 10;
Pred. No. 4.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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RESULT 8
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Best Local Similarity
Matches 101; Conserv
                                                                                         094JH3; PRELIMINARY; 094JH3; 01-DEC-2001 (TrEMBLrel. 1 01-DEC-2001 (TrEMBLrel. 1 01-MAR-2003 (TrEMBLrel. 2
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Q8LQ61;
01-OCT-2002
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                Peptidase-like protein. P0638D12.16.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003768; BAB91937.1; -. Gramene; Q8LQ61; -.
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01-MAR-2003 (TrEMBLrel.
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Sasaki T., Matsumoto T
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                                                                                                                                                                                                                                                                                                                                                                                                                  108 EYAVYHSLYDDFVWMEKFGDPLFRRHVAAASMWGLVALRLSDEEILPFNYSTYAVELEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                             240 GYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 ETQSLYDLWM----ASDSSSMIKIGRIGGGGSDYSAFVQHIGIPS-----IDISMGS
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                                                                                                                                                                                                                                  RTNTSESWRSVQHEIYRIARVINQASLVLS
                                                                                                                                                                                                                                                              KVDPSKAWGDVKRQISVAAFTVQAAAETLS 439
                                                                                                                                                                                                                                                                                              PLKVRDLNERLMMTERAFTDREGLSGRPWYKHLVY
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                              19,
19,
23,
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                                                                                           Created)
Last sequence update)
Last annotation updat
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                                                                                     Q9XH28 PRELIMINARY; PRT; 280 AA.
Q9XH28;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-NAR-2003 (TrEMBLrel. 23, Last annotation update)
F10A2.10 Protein (Putative peptidase).
F10A2.10 OR AT4G07670.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosid enursids II; Brassicales; Brassicaceae; Arabidopsis.
"The A. thaliana Genome Submitted (MAY-1999) to
                                      SEQUENCE FROM N.A. STRAIN-CV. Columbia;
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Pfam; PF04253; TFR_dimer; 1.
PROSITE; PS50840; PA; 1.
                            WASHU;
                                                                            NCBI_TaxID=3702;
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22.4%; Pred. No. 1.
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the EMBL/GenBank/DDBJ databases
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Best Local S
Matches 51
MEDINE-97298311; PubMed-9153759;
Jauniaux J.C., Poirey R.;
"Sequencing analysis of a 36.8 kb fr
reveals 26 open reading frames inclu
RBL2, PNT1, PAC1 and VPH1.";
Yeast 13:483-487(1997).
EMBL; Z75164; CAA99478.1; -.
SGD; S0005782; YOR256C.
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InterPro; IPR003137; PA.
Pfam; PF02225; PA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q08693;
Q08693;
                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23, Chromosome XV reading frame
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Joshu C., Bauer C., Hotic M.;
"The sequence of A. thaliana F10A2.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Submitted (JUL-1996) to
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                            YOR256C
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Pfam; PF02225; PA; 1.
PROSITE; PS50840; PA; 1.
PROSITE; PS50840; PA; 31115 MW;
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Pred. No. 2
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OC Euke
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pfam; pF02225; PA; 1.
pfam; pF04253; TFR_dimer; 1.
pROSITE; PS50840; PA; 1.
SEQUENCE 809 AA; 91995 MW;
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Q1-MAR-2003 (TrEMBLrel. 23, Created)

Q1-MAR-2003 (TrEMBLrel. 23, Last seq

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Transferrin receptor.
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                             the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK046228; BAC33277.1; -.
ESQUENCE 515 AA; 57341 MW; 86FC77FF66A80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTILFASWDAEEFGLLGSTEWAEDNSRLLQER------GVAYINADSSIEGNYTLR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHETVRSFGTLK-KEGWRPR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYNISMKHPQEMKTYSLSFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFSAVKNFTEIASKESERLODF-------DKSNPILLRM----MNDQLMFLERAFIDPL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IETHPLLKKF-FURNAH-GNFDISVDNVQHYGDWT----PFLANGIP-VSVISSD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDCTPLMYSLVYNLTKELKSPDEGFEGKSLYESWTKKSPSPEF-SGMPRISKLGSGNDFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GILPNRSFYKNVLFGPTLIQEDKSKNGGNVDFWTFPGVMDAIYDDD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLPDRPFYRHVIYAPS----SHNKYAGE----SFPGIYDALFDIESKVDPSKAWGDVKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11KGLLFWKK1GSEWASWTQGWENIVWSHGDG1EPSLLSINRWTWNKKLTNIGRRTCSPA
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISVAAFTVQAAAETLSE 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I:DLIGKVLHQSAALFVE
MGGSAPP----DSSWRGSIKVSYNVGPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%;
                                                                                                                 9.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                          31;
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Pred. No. 9.2e-10;
B; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D7D68C0A8C50ECB2 CRC64;
                                                                                       Score 224.5; DB 11;
Pred. No. 8e-09;
1; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                            86FC77FF66A80DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               515
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on functional
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                                                                                                                                                                                                                                                                                                                                                     Team;
                                                                                                                                                                                                                                                                                                                              annotation
                                                                                                                                                          515;
                                                                                                21;
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Best Local S
Matches 93
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Q08919;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Chromosome XVI reading frame ORF YPL176C.
TYPL176C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).

Saccharomyceta; Fungi; Ascomycota; Saccharomycotina; Saccharomycetaes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1996) to the EMBL; 273532; CAA97883.1; -. SGD; S0006097; YPL176C. InterPro; IPR003137; PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02225; PA; 1.
Pfam; PF04253; TFR_dimer; 1.
PROSITE; PS50840; PA; 1.
SEQUENCE 783 AA; 88755 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 DAEEFGLLGSTEWAEDNSKLLQERGVAYINADSSIEGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351
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                                                                                                                                                                                                                                                                                                                              491
                                                                                                                                                                                                                                                                                                                                                                                                   431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 VKFSNNL---FSGSLNDCRLDLLVQTAIRERHPVHDIVGKIEGSEQAGRAIVIAAPRNSA 430
                                                                                                                                                                                  596
                                                                                                                                                                                                                                                                                          186
                                                                                                                                             298
                                                                                                                                                                                                                                                                                                                                                                                                                                  74 VFGGIDPQSGAAVVHETVRSFGTL-KKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LKVSYNVGPGFTGNFSTQKVKMHIHST-NEVTRIYNVIGTLRGAVEPDRYVILGGHRDSW 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEEPDRYVVVGAQRDA-LGAGVAAKSSVGTGLLLKLAQVFSDMISKDGFRPSRSIIFASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVEPDRYVILGGHRDSWYFGGIDPQS--GAAVVHETVRSFG-TLKKEGWRPRRTILFASW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEGSCPARWNIDSSCK--LELSQN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rechmann S., (JUN-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                 SYGTMYPSFGTVVLLSLIQLYQEMVYKFDWKPLRNIYFISFGGSEFNEAGATELMEKRTE
                                                                                                                                                                                                                  FSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLR
                                                                                                                                                                                                                                                     HQFGDWT----PYLAQGIPVAIISSPGVMNREHPIYTVEDKFDFIKDKLRDKKKGEV--
                                                                                                                                                                                                                                                                                     YE--SWTKKSPSPEFS-GMP--RISKLGSGNDFEVFF---QRLGIASGRARYTKNWETNK
                                                                                                                                                                                                                                                                                                                            ALKSEIYTIIDVGQIGIWDDSN-----NLEIQCHPLLVDL---FQKNMTSRKFNVKVDNV
                                                                                                                                                                                                                                                                                                                                                  LSEIMLY-----LVEK-------SLELIDDPFIPFSISNYVDFL-
GESFPGIYDALFDIESKVDPSKAW--GDVKRQISVAAF-TVQAAAETLSEV
                                   TELMYGAGTY1EPTIIAINRWSWNYLLSLIGVTQCLEEGLMDRTFYKNVIFGPKLW----
                                                                                                                                           KYADKIYNISMKHPQEMKTYSLSFDSLFSAVKNFTEIASKFSERLQDFDKSNPILLRMMN
                                                                        DQLMFLERAFIDPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                          ·STTLKDLQKECPDTVNFDEVFLGTTLWENTKLQFEKWKSEW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88755 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nentwich U., Voss H., i
the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7%; Score 179.5; DB 3;
7%; Pred. No. 4.2e-05;
82; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85D78D5D2FE114A7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ansorge W.; I databases.
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                                                                              -GLPDRPFYRHVIYAPSSHNKYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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             441
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

RA Harros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,

RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,

RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

ROUTINHO L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan J.P.,

RA Fraga J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

RA Machado M.A., Madeira B.N., Madeira H.M.F., Matsukuma A.Y.,

RA Monn D. H., Narai M.R., Nascimento A. I. T. O. Natto I. F. S.

RA Monn D. H., Narai M.A., Nascimento A. I. T. O. Natto I. F. S.
                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.C.,
de Oliveira M.C., de Oliveira R.C., Pamieri D.A., Paris A.,
etixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Quaggio R.B., Roberto P.G., Rodrígues V., de Rosa A.J.M.,
de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
da Silva A.C.R., da Silva A.M., Jr., Silva W.A. Jr.,
da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
Vanilada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
                                                                                                                                                                                                                                                                                                                                                                 "The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
EMBL; AE003921; AAF83630.1; -.
                                                                                                                                                                                                                                                                                                        PROSITE; PS00287; CYSTATIN;
Hypothetical protein; Comple
SEQUENCE 529 AA; 57664 My
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20365717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xylella fastidiosa.
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                                                                                                                                                                                                                                            66;
                                                                                                                                                                                                                                                         Similarity
                                                                                                                                           TVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERGVAYINAD----
                                                QGPTRDFGIYGTAKLDLLDMLKQVAAGWKLRYTLD---PTPEAGHFFRSDHFSFAKR---
                PEFSGMPRISKLGSGNDFEVFFQRLGIASGRA
                                                                              ---SSIEGNY-TLRVDCTPLM-----YSLVYNLTKELKSPDEGFEGKSLYESWTKKSPS 195
                                                                                                             LARGEA----RGPQPQRSVLFLAVTAEEKGLLGS-EYYASNPLYPLEKTVAVINMDVMNP
                                                                                                                                                                                                            NEVTRIYNVIGTLRGAVEPDRYVILGGHRD-----SWVF-GGIDPQSGAAVVHE
                                                                                                                                                                           SEVITSHNVAARLQGCAHPDETVIYSAHWDHLGVGAPDAKGDTIFNGALDNASGTAALLE
                                                                                                                                                                                                                                                                                                                                                        IPR000010; Cystatin.
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                                                                                                                                                                                                                                                                                                           57664 MW;
                                                                                                                                                                                                                                                        7.48;
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                                                                                                                                                                                                                                                                                                   Complete proteome.
7664 MW; 37EFC71953B41655 CRC64;
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Last annotation update)
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Pred. No. 7.5e-05;
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                                                                                                                                                                                                                                                                       Length 529;
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RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 33913 / NCPPB 528;

RX MEDLINE-22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Sarah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Camargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Carelli R.M.B., Couttinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Meidanis J., Sena J.A.D., Silva C., Oliveira W.R.,

RA Spinola L.A.F., Takita M.A., Truffi D., Tsai S.M., White F.F.,

RA Spinola J.C., Kitalima J.P.,

RA Spinola J.C., Kitalima J.P.,

RA RA Martins E.C., White F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 59
                                                                                   Q9A5A8
Q9A5A8;
Q1-JUN-2001
01-JUN-2001
01-MAR-2003
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Q8P530;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE012471; AAM42787.1; -. Complete proteome. SEQUENCE 549 AA; 59295 MW;
Caulobacter crescentus
                                Aminopeptidase, putative. CC2544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                host specificities.";
Nature 417:459-463(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparison of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonadaceae;
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Setubal J.C., Kitajima J.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 LARGFA----KGPKPERSVVFLAVTAEEKGLLGSEFYA---SKPLYPLATTVAVINMDGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 NEVTRIYNVIGTLRGAVEPDRYVILGGH------RDSWVF-GGIDPQSGAAVVHE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEDNSRLLQERG--VAYINAD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDVITSHNVVARLEGSTHPDETLIYSAHWDHIGVGKPDARGDTIFNGALDNASGTAALLE
                                                                                                                                                                                                                                                                                                                                                 RSDHFSFAKR-----GVPALS-YAAGQDWEVG---
                                                                                                                                                                                                                                                                                                                                                                                                       KSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRA
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                                                                                   (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 23,
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33;
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                                                                                                                    Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SSIEGNYTLRVDCTPLMYSLVYNLTKELKSPDEGFEG
                                                                                                                                                                                                        PRT;
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Search completed: October 4, 2003, 23:25:13 Job time: 81 secs
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                                                                                                                                                                                                                                                                                                                                           Query Match 6.7%; Score 157; DB 16; Length 467; Best Local Similarity 30.3%; Pred. No. 0.0011; Matches 44; Conservative 28; Mismatches 59; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed-11259647;

MEDLINE-21173698; PubMed-11259647;

MISTIME C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Risen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Ely B.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Witterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 467 AA; 48918 MW; 9984DE2A9D84F00F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter. NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003137; PA. PROSITE; PS50840; PA; 1.
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                                                                          347 -ESDTGADRIYSLQVPAGSLDHPVV 370
                                                                                                                              142 INADSSIEGNYTLRVDCTPLMYSLV 166
                                                                                                                                                                   292 GTATTTAAAKLIGDLPK---RPKRTIRVVMWGSEESG--GSSEAYLAANKDALSTMVLAG 346
                                                                                                                                                                                                                                                           232 AARKVPMRVKLKLESSVNPNNVAWNISGDIKGSEKPDEVIVIGGHLDSWDVGTGALDDAT 291
                                                                                                                                                                                                                                                                                    83 GAAVVHETVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTE-WAEDNSRLLQERGVAY 141
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